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OM protein - protein search, using sw model

Run on: February 21, 2003, 16:11:08 : Search time 161.419 Seconds

(Without alignments)
71.895 Million cell updates/sec

Title: US-09-992-067-1

Sequence: 1 KSPQEQETVLGDLNLIIRY 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Hit number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCNUS.COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US05.COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07.COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080.COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081.COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082.COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083.COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084.COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085.COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086.COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087.COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088.COMB.pep.*
- 13: /cgn2_6/ptodata/1/paa/US089.COMB.pep.*
- 14: /cgn2_6/ptodata/1/paa/US090.COMB.pep.*
- 15: /cgn2_6/ptodata/1/paa/US091.COMB.pep.*
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- 23: /cgn2_6/ptodata/1/paa/US099.COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100.COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101.COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102.COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	18	23	US-09-992-067-1
2	91	100.0	339	1	PCT-US01-08656-10252
3	91	100.0	737	26	US-10-221-279-9937
4	91	100.0	838	27	US-60-230-445-1056
5	91	100.0	847	1	PCT-US01-14827-14550
6	91	100.0	900	1	PCT-US02-29221-2

7	91	100.0	930	21	US-09-791-537-12639	Sequence 12639, A
8	91	100.0	930	21	US-09-791-537-55361	Sequence 53361, A
9	91	100.0	930	21	US-09-791-537-118834	Sequence 118834, A
10	91	100.0	971	1	PCT-US01-14827-14552	Sequence 14552, A
11	86	94.5	123	1	PCT-US01-08656-10251	Sequence 10251, A
12	80.5	88.5	19	23	US-09-993-295-2	Sequence 2, Appl1
13	79	86.8	16	22	US-09-826-290-44	Sequence 44, Appl1
14	47.5	52.2	853	21	US-09-791-537-80386	Sequence 80386, A
15	47.5	52.2	853	21	US-09-791-537-151450	Sequence 151450, A
16	47.5	52.2	853	27	US-60-384-450-29	Sequence 29, Appl1
17	47.5	52.2	858	21	US-09-791-537-10439	Sequence 10439, A
18	47.5	52.2	858	21	US-09-791-537-116884	Sequence 116884, A
19	45	49.5	428	21	US-09-708-427-6340	Sequence 6340, Ap
20	45	49.5	428	21	US-09-708-427-6339	Sequence 6339, Ap
21	45	49.5	452	21	US-09-708-427-6338	Sequence 6338, Ap
22	44	48.4	856	21	US-09-791-537-107293	Sequence 107293, A
23	43	47.3	626	26	US-10-238-659-538	Sequence 538, App
24	43	47.3	640	26	US-10-219-999-35481	Sequence 35481, A
25	43	47.3	640	27	US-60-324-109-20944	Sequence 20944, A
26	43	47.3	946	1	PCT-US00-09678-1	Sequence 1, Appl1
27	43	47.3	946	22	US-09-828-423-3	Sequence 3, Appl1
28	43	47.3	946	25	US-10-191-988-1	Sequence 1, Appl1
29	43	47.3	946	27	US-60-389-987-2036	Sequence 2036, Ap
30	43	47.3	946	27	US-60-412-418-2036	Sequence 2036, Ap
31	42	46.2	362	21	US-09-791-537-12075	Sequence 12075, A
32	42	46.2	384	21	US-09-791-537-37888	Sequence 37888, A
33	42	46.2	497	21	US-09-791-537-104174	Sequence 104174, A
34	42	46.2	544	15	US-09-198-452A-153	Sequence 153, App
35	42	46.2	544	21	US-09-791-537-89671	Sequence 89671, A
36	42	46.2	544	21	US-09-791-537-138326	Sequence 138326, A
37	42	46.2	544	22	US-09-809-745-3	Sequence 3, Appl1
38	42	46.2	544	22	US-09-841-132-400	Sequence 400, App
39	42	46.2	535	18	US-09-438-185-136	Sequence 136, App
40	42	46.2	555	18	US-09-438-185A-136	Sequence 136, App
41	42	46.2	652	26	US-10-219-999-32066	Sequence 32066, A
42	42	46.2	652	27	US-60-324-109-17013	Sequence 17013, A
43	42	46.2	660	26	US-10-219-999-61460	Sequence 61460, A
44	42	46.2	660	27	US-60-324-109-29963	Sequence 29963, A
45	42	46.2	858	14	US-09-020-244-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-992-067-1 Application US/09992067
Sequence 1, Appl1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: Interalpha Trypsin Inhibitor Biopolymer Markers Indicative of
FILE REFERENCE: 2132.100
CURRENT APPLICATION NUMBER: US/09/992.067
CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-067-1

Query Match 100.0%; Score 91; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPQEQETVLGDLNLIIRY 18
DB 1 KSPQEQETVLGDLNLIIRY 18

RESULT 2
PCT-US01-08656-10252

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; Sequence 10252, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 10252
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (156)..(209)
; OTHER INFORMATION: INHIBITOR HEAVY CHAIN CHANNEL IN domain identified by
; OTHER INFORMATION: EMATRIX, accession number PD01101B, P-value=1.000e-40, raw score
; OTHER INFORMATION: 21.53
; NAME/KEY: DOMAIN
; LOCATION: (174)..(339)
; OTHER INFORMATION: von Willebrand factor type A domain identified by Pfam,
; OTHER INFORMATION: accession name vwa, E-value=0.00046, Pfam score of 5.5
PCT-US01-08656-10252
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Query Match          100.0%; Score 91; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KSPEQOETVLDGNLIIRY 18
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DB 124 KSPEQOETVLDGNLIIRY 141
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RESULT 3
US-10-221-279-9937
; Sequence 9937, Application US/10221279
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-046
; CURRENT APPLICATION NUMBER: US/10/221,279
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 12360
; SOFTWARE: Custom
; SEQ ID NO 9937
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-279-9937
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Query Match          100.0%; Score 91; DB 26; Length 737;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KSPEQOETVLDGNLIIRY 18
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DB 31 KSPEQOETVLDGNLIIRY 48
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RESULT 4
US-60-230-445-1056
; Sequence 1056, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
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; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: CLO00765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1056
; LENGTH: 838
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-445-1056
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Query Match          100.0%; Score 91; DB 27; Length 838;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KSPEQOETVLDGNLIIRY 18
    |||
DB 224 KSPEQOETVLDGNLIIRY 241
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```
RESULT 5
PCT-US01-14827-14550
; Sequence 14550, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 14550
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (256)..(309)
; OTHER INFORMATION: INHIBITOR HEAVY CHAIN CHANNEL IN domain identified by
; OTHER INFORMATION: EMATRIX, accession number PD01101B, P-value=1.000e-40, raw sco
; NAME/KEY: DOMAIN
; LOCATION: (274)..(457)
; OTHER INFORMATION: von Willebrand factor type A domain identified by Pfam,
; OTHER INFORMATION: accession name vwa, E-value=1.1e-08, Pfam score of 42.3
PCT-US01-14827-14550
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Query Match          100.0%; Score 91; DB 1; Length 847;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KSPEQOETVLDGNLIIRY 18
    |||
DB 224 KSPEQOETVLDGNLIIRY 241
```

```
RESULT 6
PCT-US02-29221-2
; Sequence 2, Application PC/TUS0229221
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SPRAGUE, William W.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: LI, Joana X.
```

```

: APPLICANT: GRIFFIN, Jennifer A.
: APPLICANT: GIETZEN, Kimberly J.
: APPLICANT: YANG, Junming
: APPLICANT: LU, Dyrung Alina M.
: APPLICANT: EMERLING, Brooke M.
: APPLICANT: DUGGAN, Brendan M.
: APPLICANT: RICHARDSON, Thomas W.
: APPLICANT: LEE, Soo Yeun
: APPLICANT: RAMKUMAR, Jayalaxmi
: APPLICANT: BECHA, Shanya D.
: APPLICANT: LEHR-MASON, Patricia M.
: APPLICANT: SMARNAKAR, Anita
: APPLICANT: TRAN, Uyen K.
: APPLICANT: KABLE, Amy E.
: APPLICANT: HAFALIA, April J.A.
: TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
: FILE REFERENCE: PF-1186 PCT
: CURRENT APPLICATION NUMBER: PCT/US02/29221
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: US 60/322,196
: PRIOR FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: US 60/324,134
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: US 60/327,233
: PRIOR FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: US 60/346,198
: PRIOR FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: US 60/343,980
: PRIOR FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: US 60/348,887
: PRIOR FILING DATE: 2001-11-09
: PRIOR APPLICATION NUMBER: US 60/332,423
: PRIOR FILING DATE: 2001-11-16
: PRIOR APPLICATION NUMBER: US 60/334,145
: PRIOR FILING DATE: 2001-11-28
: PRIOR APPLICATION NUMBER: US 60/334,229
: PRIOR FILING DATE: 2001-11-28
: PRIOR APPLICATION NUMBER: US 60/337,451
: PRIOR FILING DATE: 2001-12-06
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 62
: SOFTWARE: PERL Program
: SEQ ID NO 2
: LENGTH: 900
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 7500515CD1
PCT-US02-29221-2

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Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KSPSEQETVLDGNLIIRY 18
Db      224 KSPSEQETVLDGNLIIRY 241

RESULT 7
US-09-791-537-12639
: Sequence 12639, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Biomimix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
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: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: patentin version 3.0
: SEQ ID NO 12639
: LENGTH: 930
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-537-12639

Query Match          100.0%; Score 91; DB 21: Length 930;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KSPSEQETVLDGNLIIRY 18
Db      224 KSPSEQETVLDGNLIIRY 241

RESULT 8
US-09-791-537-53361
: Sequence 53361, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Biomimix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 53361
: LENGTH: 930
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-537-53361

Query Match          100.0%; Score 91; DB 21: Length 930;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KSPSEQETVLDGNLIIRY 18
Db      224 KSPSEQETVLDGNLIIRY 241

RESULT 9
US-09-791-537-118834
: Sequence 118834, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Biomimix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 118834
: LENGTH: 930
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-537-118834

Query Match          100.0%; Score 91; DB 21: Length 930;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KSPSEQETVLDGNLIIRY 18
Db      224 KSPSEQETVLDGNLIIRY 241
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RESULT 10
PCT-US01-14827-14552
; Sequence 14552, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 14552
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (295)..(348)
; OTHER INFORMATION: INHIBITOR HEAVY CHAIN CHANNEL IN domain identified by
; OTHER INFORMATION: EMATRIX, accession number PD01101B, P-value=1.000e-40, raw score
; OTHER INFORMATION: 21.53
; NAME/KEY: DOMAIN
; LOCATION: (313)..(496)
; OTHER INFORMATION: von Willebrand factor type A domain identified by Pfam,
; OTHER INFORMATION: accession name vwa, E-value=1.1e-08, Pfam score of 42.3
PCT-US01-14827-14552

Query Match 100.0%; Score 91; DB 1; Length 971;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPEQOETVLDGNLIIRY 18
Db 263 KSPEQOETVLDGNLIIRY 280

RESULT 11
PCT-US01-08656-10251
; Sequence 10251, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 10251
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08656-10251

Query Match 94.5%; Score 86; DB 1; Length 123;
Best Local Similarity 94.4%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSPEQOETVLDGNLIIRY 18
Db 53 KSPEQOETVLDGNLIIRY 70

RESULT 12
US-09-993-295-2
; Sequence 2, Application US/09993295

; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Macroglobulin Biopolymer Markers Indicative of Insulin Resista
; FILE REFERENCE: 2132,099
; CURRENT APPLICATION NUMBER: US/09/993,295
; CURRENT FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-295-2

Query Match 88.5%; Score 80.5; DB 23; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KSPEQOETVLDGNLIIRY 18
Db 1 KSPEQOETVLDGNLIIRY 19

RESULT 13
US-09-826-290-44
; Sequence 44, Application US/09826290
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stieger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-44

Query Match 86.8%; Score 79; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPEQOETVLDGNLIIR 17
Db 1 SPEQOETVLDGNLIIR 16

RESULT 14
US-09-791-537-83086
; Sequence 83086, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek

```

: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 83086
: LENGTH: 853
: TYPE: PRT
: ORGANISM: Bos taurus
: US-09-791-537-83086

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Query Match          52.2%; Score 47.5; DB 21; Length 853;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 5; Mismatches 0; Indels 1; Gaps 1;

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QY      3 PEOQETVLDGNLIIR 17
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      358 PEOQET-LDGHMYYR 371

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RESULT 15
: US-09-791-537-151450
: Sequence 151450. Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Blomomix, Inc.
: APPLICANT: Danze, Derek
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 151450
: LENGTH: 853
: TYPE: PRT
: ORGANISM: Bos taurus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (556)..(556)
: OTHER INFORMATION: X is an unknown amino acid
: US-09-791-537-151450

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Query Match          52.2%; Score 47.5; DB 21; Length 853;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 5; Mismatches 0; Indels 1; Gaps 1;

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QY      3 PEOQETVLDGNLIIR 17
      ||||| |||:::|
      358 PEOQET-LDGHMYYR 371

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Search completed: February 21, 2003, 16:19:46
Job time : 174.419 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2003, 16:10:02 : Search time 10.0645 Seconds
(without alignments)
38.005 Million cell updates/sec

Title: US-09-992-067-2
Perfect score: 75
Sequence: 1 KOHRCIDSGAGRN 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	614	1	US-08-543-881-2
2	75	100.0	614	1	US-08-291-299-2
3	75	100.0	614	5	PCT-US94-00119-2
4	75	100.0	614	5	PCT-US95-10579-2
5	38	50.7	154	3	US-08-244-113-7
6	38	50.7	154	3	US-08-973-068-9
7	38	50.7	237	6	5212074-7
8	37	49.3	166	1	US-07-781-254A-21
9	37	49.3	256	4	US-09-077-955-30
10	37	49.3	294	4	US-09-077-955-28
11	37	49.3	338	4	US-09-077-955-28
12	37	49.3	390	4	US-09-077-955-27
13	37	49.3	440	4	US-09-077-955-26
14	37	49.3	444	1	US-07-626-618A-20
15	37	49.3	444	1	US-08-333-977-20
16	37	49.3	446	1	US-07-781-254A-2
17	37	49.3	446	1	US-07-781-254A-3
18	37	49.3	456	4	US-09-077-955-25
19	37	49.3	492	2	US-08-644-271-32
20	37	49.3	492	4	US-09-077-955-36
21	37	49.3	656	3	US-08-738-000-4
22	37	49.3	656	4	US-09-258-928-4
23	37	49.3	656	4	US-09-347-878-24
24	37	49.3	660	3	US-08-738-000-2
25	37	49.3	660	4	US-09-258-928-2
26	36	48.0	41	6	5208144-18
27	36	48.0	88	1	US-08-440-103-26

28	36	48.0	88	1	US-08-440-103-27	Sequence 27, Appl
29	36	48.0	88	1	US-08-440-542-26	Sequence 26, Appl
30	36	48.0	88	1	US-08-440-542-27	Sequence 27, Appl
31	36	48.0	88	1	US-08-231-368-26	Sequence 26, Appl
32	36	48.0	88	1	US-08-231-368-27	Sequence 26, Appl
33	36	48.0	88	1	US-08-440-210-26	Sequence 26, Appl
34	36	48.0	88	1	US-08-440-210-27	Sequence 26, Appl
35	36	48.0	88	4	US-09-046-604-26	Sequence 26, Appl
36	36	48.0	88	4	US-09-046-604-27	Sequence 27, Appl
37	36	48.0	129	4	US-09-199-637A-371	Sequence 37, Appl
38	36	48.0	179	4	US-08-444-818-77	Sequence 77, Appl
39	36	48.0	255	4	US-09-134-001C-3498	Sequence 3498, Ap
40	36	48.0	329	1	US-07-991-587A-7	Sequence 7, Appl
41	36	48.0	329	1	US-08-309-985-7	Sequence 7, Appl
42	36	48.0	332	1	US-08-446-875-12	Sequence 12, Appl
43	36	48.0	332	2	US-08-102-385G-12	Sequence 12, Appl
44	36	48.0	353	1	US-08-440-103-31	Sequence 31, Appl
45	36	48.0	353	1	US-08-440-542-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-543-881-2
; Sequence 2, Application US/08543881
; Patent No. 5712148
; GENERAL INFORMATION:
; APPLICANT: Borden, Laurence A.
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinsbank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAININE/GABA TRANSPORTER
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,881
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,858
; FILING DATE:
; APPLICATION NUMBER: US/08/001,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P. John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897/JPW/KEK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: procein
; US-08-543-881-2
Query Match 100.0%; Score 75; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOHPCLDGSAGR 13
| | | | |
Db 583 KOHPCLDGSAGR 595

RESULT 2

US-08-291-299-2
; Sequence 2, Application US/08291299
; Patent No. 5766848
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINNE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,299
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-291-299-2

Query Match

Best Local Similarity 100.0%; Score 75; DB 1; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOHPCLDGSAGR 13
| | | | |
Db 583 KOHPCLDGSAGR 595

RESULT 3

PCT-US94-00119-2
; Sequence 2, Application PC/TUS9400119
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINNE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00119
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: 42897-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-00119-2

PCT-US94-00119-2

Query Match 100.0%; Score 75; DB 5; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOHPCLDGSAGR 13
| | | | |
Db 583 KOHPCLDGSAGR 595

RESULT 4

PCT-US95-10579-2
; Sequence 2, Application PC/TUS9510579
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A HUMAN BETAINNE/GABA
; TITLE OF INVENTION: TRANSPORTER AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10579
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42897-A-PCT/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-10579-2

PCT-US95-10579-2

Query Match 100.0%; Score 75; DB 5; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOHPCLOSSAGRN 13
 Db 583 KOHPCLOSSAGRN 595

RESULT 5

US-08-244-113-7
 ; Sequence 7, Application US/08244113
 ; Patent No. 5455181
 ; GENERAL INFORMATION:
 ; APPLICANT: Strube, Karl-Hermann
 ; APPLICANT: Bialojan, Siegfried
 ; APPLICANT: Kroege, Burkhard
 ; APPLICANT: Friedlich, Thomas
 ; TITLE OF INVENTION: No. 5455181el thrombin-inhibitory proteins from terrestrial
 ; TITLE OF INVENTION: leeches.
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kell & Weinkauff
 ; STREET: 1101 Connecticut Avenue
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM AT-compatible, 80486 processor
 ; OPERATING SYSTEM: MS-DOS version 6.0
 ; SOFTWARE: WordPerfect version 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/244,113
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; CLASSIFICATION: C07K 73/10
 ; CLASSIFICATION: A61K 37/64
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP92/02661
 ; FILING DATE: 19-NOV-1992
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-244-113-7

Query Match 50.7%; Score 38; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PCLDGSAG 11
 Db 9 PCLDGSAG 16

RESULT 6

US-08-973-068-9
 ; Sequence 9, Application US/08973068
 ; Patent No. 6127604
 ; GENERAL INFORMATION:
 ; APPLICANT: Dale, James Langham
 ; APPLICANT: Harding, Robert Maxwell
 ; APPLICANT: Dugdale, Benjamin
 ; APPLICANT: Beecham, Peter Ronald
 ; APPLICANT: Hafner, Gregory John
 ; APPLICANT: Becker, Douglas Kenneth
 ; TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
 ; FILE REFERENCE: 09657/002001
 ; CURRENT APPLICATION NUMBER: US/08/973,068
 ; CURRENT FILING DATE: 1998-03-12
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00335
 ; EARLIER FILING DATE: 1996-05-31

NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Banana Bunchy Top Virus (BBTV)
 ; US-08-973-068-9

Query Match 50.7%; Score 38; DB 3; Length 154;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 PCLDGSAG 12
 Db 32 PCVDSGAGR 40

RESULT 7

5212074-7
 ; Patent No. 5212074
 ; APPLICANT: KIEFER, MICHAEL C.; MASTARZ, FRANK R.
 ; TITLE OF INVENTION: GENETIC MATERIAL ENCODING NEW
 ; INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN IGFBP-6
 ; NUMBER OF SEQUENCES: 7
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/576,629
 ; FILING DATE: 31-AUG-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 574,613
 ; FILING DATE: 28-AUG-1990
 ; SEQ ID NO: 7:
 ; LENGTH: 237
 ; 5212074-7

Query Match 50.7%; Score 38; DB 6; Length 237;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSAGR 12
 Db 195 HPALDGGGRK 204

RESULT 8

US-07-781-254A-21
 ; Sequence 21, Application US/07781254A
 ; Patent No. 5407823
 ; GENERAL INFORMATION:
 ; APPLICANT: Sokoloff, Pierre
 ; APPLICANT: Martress, Marie-Pascale
 ; APPLICANT: Schwartz, Jean-Charles
 ; APPLICANT: Giros, Bruno
 ; TITLE OF INVENTION: Polypeptides Having a Dopaminergic Receptor
 ; TITLE OF INVENTION: Activity, Nucleic Acids Coding for These Polypeptides and th
 ; TITLE OF INVENTION: Use of These Polypeptides for the Screening of Substances
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 3100 No. 5407823west Center
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/07/781,254A
 ; FILING DATE: 31-DEC-1991
 ; CLASSIFICATION: 530

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ATTORNEY/AGENT INFORMATION:
; NAME: Hillson, Randall A.
; REGISTRATION NUMBER: 31,939
; REFERENCE/DOCKET NUMBER: 8076.51-MOUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Variant D-3 dopaminergic receptor peptide
; CLONE: (210-375)
; US-07-781-254A-21

Query Match      49.3%; Score 37; DB 1; Length 166;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 OHPCLDGSAG 11
      1111111111
DB      103 RHPSLEGAG 112

RESULT 9
US-09-077-955-30
; Sequence 30, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-077-955-30

Query Match      49.3%; Score 37; DB 4; Length 256;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 HPCLDGSA 10
      1111111111
DB      27 HPLCNGAS 34

RESULT 10
US-09-077-955-29
; Sequence 29, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
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; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 29
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-077-955-29

Query Match      49.3%; Score 37; DB 4; Length 294;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 HPCLDGSA 10
      1111111111
DB      65 HPLCNGAS 72

RESULT 11
US-09-077-955-28
; Sequence 28, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 28
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-077-955-28

Query Match      49.3%; Score 37; DB 4; Length 338;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 HPCLDGSA 10
      1111111111
DB      109 HPLCNGAS 116

RESULT 12
US-09-077-955-27
; Sequence 27, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 390
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-077-955-27

Query Match
Best Local Similarity 49.3%; Score 37; DB 4; Length 390;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HPCLDGSA 10
161 HPCLDGSA 168

RESULT 13
US-09-077-955-26

Sequence 26, Application US/09077955A
Patent No. 6413740
GENERAL INFORMATION:
APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 440
TYPE: PRT
ORGANISM: Homo sapiens
US-09-077-955-26

Query Match
Best Local Similarity 49.3%; Score 37; DB 4; Length 440;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HPCLDGSA 10
211 HPCLDGSA 218

RESULT 14

US-07-626-618A-20
Sequence 20, Application US/07626618A
Patent No. 5422265

GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civeilli, Olivier
TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/626,618A
FILING DATE: 7 DEC 1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5422265nan, Kevin E

REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-07-626-618A-20

Query Match
Best Local Similarity 49.3%; Score 37; DB 1; Length 444;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHPCLDGSA 11
310 RHPSLGGAG 319

RESULT 15
US-08-333-977-20

Sequence 20, Application US/08333977
Patent No. 5594108
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civeilli, Olivier
TITLE OF INVENTION: A No. 5594108el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,977
FILING DATE: 03-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,618
FILING DATE: 7 DEC 1990
ATTORNEY/AGENT INFORMATION:
NAME: No. 5594108nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-333-977-20

Query Match
Best Local Similarity 49.3%; Score 37; DB 1; Length 444;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHPCLDGSAG 11
:111:111
Db 310 RHPLEGAG 319

Search completed: February 21, 2003, 16:14:51
Job time : 11.0645 secs


```
; Sequence 3, Application US/09993295
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Macroglobulin Biopolymer Markers Indicative of Insulin Resistance
; FILE REFERENCE: 2132.099
; CURRENT APPLICATION NUMBER: US/09/993,295
; CURRENT FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-295-3

Query Match
Best Local Similarity 100.0%; Score 75; DB 23; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGR 13
| | | | | | | | | | | | |
; 1 KOHPCLDGSAGR 13

RESULT 3
US-60-230-445-1802
; Sequence 1802, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO00765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1802
; LENGTH: 244
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-445-1802

Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 244;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGR 13
| | | | | | | | | | | | |
; 213 KOHPCLDGSAGR 225

RESULT 4
US-60-230-445-1725
; Sequence 1725, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO00765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1725
; LENGTH: 499
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-445-1725

Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 499;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGR 13
| | | | | | | | | | | | |
; 213 KOHPCLDGSAGR 225

; Sequence 3, Application US/09993295
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Macroglobulin Biopolymer Markers Indicative of Insulin Resistance
; FILE REFERENCE: 2132.099
; CURRENT APPLICATION NUMBER: US/09/993,295
; CURRENT FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-295-3

Query Match
Best Local Similarity 100.0%; Score 75; DB 23; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGR 13
| | | | | | | | | | | | |
; 1 KOHPCLDGSAGR 13

RESULT 5
US-09-018-436-2
; Sequence 2, Application US/09018436
; GENERAL INFORMATION:
; APPLICANT: Borden, Laurence A.
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinstanek, Richard L.
; TITLE OF INVENTION: Method for Identifying Compounds Which
; TITLE OF INVENTION: Specifically Bind A Human Betaine/GABA Transporter
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Ave of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,436
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/42897-AZ/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-018-436-2

Query Match
Best Local Similarity 100.0%; Score 75; DB 14; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGR 13
| | | | | | | | | | | | |
; 583 KOHPCLDGSAGR 595

RESULT 6
US-09-919-039-378
; Sequence 378, Application US/09919039
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 378
; LENGTH: 614
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 5834958CD1
US-09-919-039-378
```

```
Query Match
Best Local Similarity 100.0%; Score 75; DB 23; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 KOHPCLDGSAGRN 13
Db 583 KOHPCLDGSAGRN 595
```

```
RESULT 7
US-60-208-973-196
; Sequence 196, Application US/60208973
; GENERAL INFORMATION:
```

```
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: C1000638
CURRENT APPLICATION NUMBER: US/60/208,973
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 264
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 196
LENGTH: 614
TYPE: PRT
ORGANISM: HUMAN
US-60-208-973-196
```

```
Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 KOHPCLDGSAGRN 13
Db 583 KOHPCLDGSAGRN 595
```

```
RESULT 8
US-60-213-177-593
; Sequence 593, Application US/60213177
; GENERAL INFORMATION:
```

```
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: C1000688
CURRENT APPLICATION NUMBER: US/60/213,177
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 1266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 593
LENGTH: 614
TYPE: PRT
ORGANISM: Human
US-60-213-177-593
```

```
Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 KOHPCLDGSAGRN 13
Db 583 KOHPCLDGSAGRN 595
```

```
RESULT 9
US-60-222-113-378
```

```
; Sequence 378, Application US/60222113
; GENERAL INFORMATION:
```

```
APPLICANT: Kaaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 P
CURRENT APPLICATION NUMBER: US/60/222,113
CURRENT FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 378
LENGTH: 614
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 5834958CD1
US-60-222-113-378
```

```
Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 614;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 KOHPCLDGSAGRN 13
Db 583 KOHPCLDGSAGRN 595
```

```
RESULT 10
US-60-258-275-396
; Sequence 396, Application US/60258275
; GENERAL INFORMATION:
```

```
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: C1001026-PROV
CURRENT APPLICATION NUMBER: US/60/258,275
CURRENT FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 717
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 396
LENGTH: 634
TYPE: PRT
ORGANISM: HUMAN
US-60-258-275-396
```

```
Query Match
Best Local Similarity 100.0%; Score 75; DB 27; Length 634;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 KOHPCLDGSAGRN 13
Db 603 KOHPCLDGSAGRN 615
```

```
RESULT 11
US-60-207-583-567
; Sequence 567, Application US/60207583
; GENERAL INFORMATION:
```

```
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: C1000598
CURRENT APPLICATION NUMBER: US/60/207,583
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 664
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 567
LENGTH: 1534
TYPE: PRT
ORGANISM: HUMAN
US-60-207-583-567
```

Query Match 100.0%; Score 75; DB 27; Length 1534;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
|||||

DB 1416 KOHPCLDGSAGRN 1428

RESULT 12
US-60-230-445-1103
; Sequence 1103, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1103
; LENGTH: 1534
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-445-1103

Query Match 100.0%; Score 75; DB 27; Length 1534;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
|||||

DB 1416 KOHPCLDGSAGRN 1428

RESULT 13
US-60-207-583-336
; Sequence 336, Application US/60207583
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00598
; CURRENT APPLICATION NUMBER: US/60/207,583
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 336
; LENGTH: 1668
; TYPE: PRT
; ORGANISM: HUMAN
US-60-207-583-336

Query Match 100.0%; Score 75; DB 27; Length 1668;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
|||||

DB 1550 KOHPCLDGSAGRN 1562

RESULT 14
US-60-230-445-1804
; Sequence 1804, Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1804
; LENGTH: 1668
; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-445-1804

Query Match 100.0%; Score 75; DB 27; Length 1668;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
|||||

DB 1550 KOHPCLDGSAGRN 1562

RESULT 15
PCT-US01-08631-51701
; Sequence 51701, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/549,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 51701
; LENGTH: 1923
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1197)..(1224)
; OTHER INFORMATION: SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE domain identified
; OTHER INFORMATION: by EMATRIX, accession number PR00176c, p-value=1.000e-24, raw
; OTHER INFORMATION: score of 10.84
; NAME/KEY: DOMAIN
; LOCATION: (298)..(1658)
; OTHER INFORMATION: Sodium:neurotransmitter symporter family domain identified by
; OTHER INFORMATION: Pfam, accession name SNF, E-value=0, Pfam score of 2456.9
; NAME/KEY: misc_feature
; LOCATION: (1)...(1923)
; OTHER INFORMATION: Xaa or * as defined in Table 2
PCT-US01-08631-51701

Query Match 100.0%; Score 75; DB 1; Length 1923;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
|||||

DB 1664 KOHPCLDGSAGRN 1676

Search completed: February 21, 2003, 16:19:48
Job time: 118.581 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 21, 2003, 16:09:26 : Search time 11.7419 Seconds
(Without alignments)
106.435 Million cell updates/sec

Title: US-09-992-067-2
Perfect score: 75
Sequence: 1 K0HPCLDGSAGRN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	614	2	S68236 betaine/GABA trans
2	42	56.0	259	2	T34736 probable gas vesic
3	41.3	55.3	576	2	A84898 hypothetical prote
4	40.5	54.0	331	2	A86278 hypothetical prote
5	40	53.3	654	2	B84690 hypothetical prote
6	39	52.0	251	2	AD1145 cyclase Hisf homol
7	39	52.0	251	2	AD1504 cyclase Hisf homol
8	39	52.0	261	2	S75631 cyclase Hisf homol
9	39	52.0	445	2	E84714 probable protein k
10	39	52.0	1891	2	T43262 calcium channel al
11	39	52.0	4660	2	T42737 gp330 protein prec
12	38	50.7	207	2	E69085 conserved hypothet
13	38	50.7	237	2	I47031 insulin-like growt
14	38	50.7	251	2	F89785 formate acetyltran
15	38	50.7	254	2	I48599 insulin-like growt
16	38	50.7	254	2	I48603 insulin-like growt
17	38	50.7	254	2	JC1464 insulin-like growt
18	38	50.7	258	1	B37252 insulin-like growt
19	38	50.7	258	2	A45403 insulin-like growt
20	38	50.7	259	2	AH2167 lundazoleglycerol-
21	38	50.7	432	2	T27180 hypothetical prote
22	38	50.7	471	2	T15394 hypothetical prote
23	38	50.7	903	2	S67315 endopeptidase c1p
24	38	50.7	903	2	E88221 protein T01h3.2 [i
25	38	50.7	980	2	T24336 hypothetical prote
26	38	50.7	1538	2	H70846 hypothetical glyci
27	38	50.7	2136	2	B84651 hypothetical prote
28	37.5	50.0	561	2	T36084 hypothetical prote
29	37	49.3	284	2	C71507 probable l2 riboso

30	37	49.3	284	2	A81661 ribosomal protein
31	37	49.3	416	2	S46454 5.10-methyleneetr
32	37	49.3	446	1	D4RND3 dopamine receptor
33	37	49.3	581	2	JC7086 F2D10 protein - hu
34	37	49.3	2139	2	A35672 crumbs protein - f
35	37	49.3	2318	2	S45306 notch 3 protein - f
36	37	49.3	2321	2	S78549 notch3 protein - h
37	37	49.3	2599	2	A96616 unknown protein FI
38	36	48.0	193	2	F64158 hypothetical prote
39	36	48.0	253	2	T25768 hypothetical prote
40	36	48.0	325	2	T18594 hypothetical prote
41	36	48.0	329	2	A48715 gal-beta(1-3/1-4)G
42	36	48.0	332	2	C87426 cysteine synthase
43	36	48.0	332	2	A49879 alpha-2,3-sialyltr
44	36	48.0	416	2	E83590 cytosine permease
45	36	48.0	460	2	A12218 hypothetical prote

ALIGNMENTS

RESULT 1
S68236
betaine/GABA transport protein BGT-1 - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S68236; I56522
R:Rasola, A.; Gallietta, L.J.V.; Barone, V.; Romeo, G.; Bagnasco, S.
FEBS Lett. 373, 229-233, 1995
A:Title: Molecular cloning and functional characterization of a GABA/betaine transpor
A:Reference number: S68236; MUID:96033979; PMID:7589472
A:Accession: S68236
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-614 <RAS>
A:Cross-references: EMBL:U27699; NID:9881474; PIDN:AAA87029.1; PID:9881475
R:Border, L.A.; Smith, K.E.; Gustafson, E.L.; Branchek, T.A.; Weinsank, R.L.
J. Neurochem. 64, 977-984, 1995
A:Title: Cloning and expression of a betaine/GABA transporter from human brain.
A:Reference number: I56522; MUID:95165166; PMID:7861179
A:Accession: I56522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-9,'Y',11-570,'QL',573-614 <RES>
A:Cross-references: GB:I42300; NID:9808695; PIDN:AAA6574.1; PID:9808696
C:Genetics:
A:Gene: BGT-1
A:Map position: 12p13
C:Superfamily: gamma-aminobutyric acid transporter
F:Keywords: glycoprotein; phosphoprotein; transmembrane protein
F:45-65/Domain: transmembrane #status predicted <TM1>
F:72-92/Domain: transmembrane #status predicted <TM2>
F:116-137/Domain: transmembrane #status predicted <TM3>
F:213-232/Domain: transmembrane #status predicted <TM4>
F:238-260/Domain: transmembrane #status predicted <TM5>
F:287-307/Domain: transmembrane #status predicted <TM6>
F:321-340/Domain: transmembrane #status predicted <TM7>
F:373-393/Domain: transmembrane #status predicted <TM8>
F:423-440/Domain: transmembrane #status predicted <TM9>
F:456-476/Domain: transmembrane #status predicted <TM10>
F:496-517/Domain: transmembrane #status predicted <TM11>
F:538-559/Domain: transmembrane #status predicted <TM12>
F:40-235/Binding site: phosphate (Thr) (covalent) #status predicted
F:171,183/Binding site: carboxylate (Asn) (covalent) #status predicted
F:418/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 K0HPCLDGSAGRN 13
Db 583 K0HPCLDGSAGRN 595

RESULT 2
T34736
probable gas vesicle protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
C:Accession: T34736
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21555
A:Accession: T34736
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-259 <SEED>
A:Cross-References: EMBL:AL033505; PIDN:CAA22043.1; GSPDB:GN00070; SCOEDB:SC1E6.15
C:Genetics:
A:Gene: gvpL; SCOEDB:SC1E6.15

Query Match
Best Local Similarity 56.0%; Score 42; DB 2; Length 259;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 QHPCLDGSAGRN 13
| | | | |
Db 196 QNPRLSGAGRN 207

RESULT 3
A84898
hypothetical protein At2g46040 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84898
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-576 <STO>
A:Cross-References: GB:AE002093; NID:g3702342; PIDN:AAC62899.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46040
A:Map position: 2
Superfamily: Arabidopsis thaliana hypothetical protein F25E4.20

Query Match
Best Local Similarity 55.3%; Score 41.5; DB 2; Length 576;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 KOHPCL-DGSAG 11
| | | | |
Db 327 KMHPCLYDSAG 338

RESULT 4
A86278
hypothetical protein F14L17.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: A86278
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaytin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86278

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <STO>
A:Cross-References: GB:AE005172; NID:g7262678; PIDN:AAF43936.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match
Best Local Similarity 54.0%; Score 40.5; DB 2; Length 331;
Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 1;

OY 1 KOHP-----CLDGSAGRN 13
| | | | |
Db 238 KOHPEAMDLMYCLGAGVGN 259

RESULT 5
B84690
hypothetical protein At2g28890 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84690
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84690
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-654 <STO>
A:Cross-References: GB:AE002093; NID:g3927836; PIDN:AAC79593.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g28890
A:Map position: 2

Query Match
Best Local Similarity 53.3%; Score 40; DB 2; Length 654;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOHPCLDGSAGRN 13
| | | | |
Db 7 KLSKCLTGAGRN 19

RESULT 6
AD1145
cyclase hlsf homolog hlsf [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AD1145
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussuguet, O.; Entlian, K.D.; Fsthl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maducno, E.; Maltournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tlerréz, A.; Vazquez-Bolado, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1145
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <GLA>
A:Cross-References: GB:NC_003210; PIDN:CAC98642.1; PID:g16409939; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hlsf

C:Superfamily: cyclase hisf

Query Match 52.0%; Score 39; DB 2; Length 251;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PCLDGSAGR 12
|||||
8 PCLDVTAGR 16

RESULT 7

AD1504
cyclase hisf homolog hisf [imported] - *Listeria innocua* (strain CL1p1262)

C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text-change 14-Dec-2001
C:Accession: AD1504
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kunz, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schueller, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95804.1; PID:q16413012; GSPDB:GN00178
A:Experimental source: strain CL1p1262
C:Genetics:
A:Gene: hisf
C:Superfamily: cyclase hisf

Query Match 52.0%; Score 39; DB 2; Length 251;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PCLDGSAGR 12
|||||
8 PCLDVTAGR 16

RESULT 8

S75631
cyclase hisf - *Synechocystis* sp. (strain PCC 6803)

C:Alternate names: protein s11893
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text-change 20-Jun-2000
C:Accession: S75631
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Oikawa, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-116, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
S:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75631
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <KAN>
A:Cross-references: EMBL:ID90912; GB:AB001339; NID:q1653228; PIDN:BA18192.1; PID:q165327
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: hisf
C:Superfamily: cyclase hisf

Query Match 52.0%; Score 39; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PCLDGSAGR 12

DB 9 PCLDVNAGR 17
|||||

RESULT 9

E84714
probable protein kinase [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text-change 02-Feb-2001
C:Accession: E84714
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: E84714
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: GB:AE002093; NID:q3201634; PIDN:AAC20728.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g30940
A:Map position: 2

Query Match 52.0%; Score 39; DB 2; Length 445;
Best Local Similarity 72.7%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSAGR 13
| | | | |
DB 249 HEMLMGSGRN 259

RESULT 10

T43262
calcium channel alpha-1 chain, L-type - *Stylophora pistillata*

C:Species: *Stylophora pistillata*
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text-change 18-Feb-2000
C:Accession: T43262
R:Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert Gene 227, 157-167, 1999
A:Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, *Stylophora pistillata*.
A:Reference number: Z22375; MUID:99148007; PMID:10023047
A:Accession: T43262
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1891 <ZOC>
A:Cross-references: EMBL:U64465; NID:q4204977; PID:q4204978; PIDN:AMD11470.1
C:Genetics:
A:Gene: CACHL
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

OY 3 HPCLDGSAG 11
||| |||
DB 259 HPCSSGSSG 267

RESULT 11

T42737
gp330 protein precursor - rat

N:Alternate names: megalin
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text-change 04-Mar-2000
C:Accession: T42737
R:Salto, A.; Pietromonaco, S.; Loo, A.K.C.; Farguhar, M.G. Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A:Title: Complete cloning and sequencing of rat gp330/megalyn, a distinctive member o
A:Reference number: A58173; MUID:95024033; PMID:7937880

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: February 21, 2003, 16:03:36 : Search time 13.4194 Seconds

(without alignments)
40.180 Million cell updates/sec

Title: US-09-992-067-2

Sequence: 1 KOHPCLDGSAGRN 13

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	614	1	S6AC_HUMAN
2	39	52.0	251	1	HIS6_LISIN
3	39	52.0	251	1	HIS6_LISMO
4	39	52.0	261	1	HIS6_SYNY3
5	39	52.0	4660	1	LRP2_RAT
6	38	50.7	232	1	SAX1_CHICK
7	38	50.7	237	1	IBP4_SHEEP
8	38	50.7	254	1	IBP4_MOUSE
9	38	50.7	258	1	IBP4_MOUSE
10	38	50.7	258	1	IBP4_MOUSE
11	38	50.7	258	1	IBP4_MOUSE
12	38	50.7	259	1	IBP4_MOUSE
13	38	50.7	471	1	HIS6_ANASP
14	38	50.7	580	1	RGPI_XENLA
15	38	50.7	811	1	HSP7_YEAST
16	38	50.7	942	1	MSH2_MAZE
17	37	49.3	284	1	RL2_CHLMD
18	37	49.3	284	1	RL2_CHLMD
19	37	49.3	446	1	D3DR_RAT
20	37	49.3	456	1	COLO_HUMAN
21	37	49.3	581	1	COLO_HUMAN
22	37	49.3	656	1	MTNR_HUMAN
23	37	49.3	2139	1	MTNR_HUMAN
24	37	49.3	2318	1	NTC3_MOUSE
25	37	49.3	2319	1	NTC3_MOUSE
26	37	49.3	2321	1	NTC3_MOUSE
27	36	48.0	193	1	YHMF_HAEIN
28	36	48.0	333	1	YHMF_HAEIN
29	36	48.0	349	1	CTGF_BOVIN
30	36	48.0	475	1	CTGF_BOVIN
31	36	48.0	830	1	FA10_CHICK
32	36	48.0	854	1	SREC_HUMAN
33	36	48.0	1816	1	UN33_CAEL

34	36	48.0	3011	1	POLG_HCV1
35	36	48.0	4486	1	DYH9_HUMAN
36	35	47.3	235	1	PRXB_YEAST
37	35	46.7	104	1	RK21_PORPU
38	35	46.7	300	1	Y921_METJA
39	35	46.7	351	1	COB1_METJA
40	35	46.7	362	1	HUG1_HUMAN
41	35	46.7	402	1	SYT7_HUMAN
42	35	46.7	403	1	SYT7_MOUSE
43	35	46.7	471	1	MANC_SALMO
44	35	46.7	499	1	ACH3_RAT
45	35	46.7	501	1	VL1_RHPV1

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	614 AA.
AC	S6AC_HUMAN				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Sodium- and chloride-dependent betaine transporter (Na+/Cl- betaine/GABA transporter) (BGT-1).				
GN	SLC6A12.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=96033979; PubMed=7589472;				
RA	Rasola A., Galietta L.J.V., Barone V., Romeo G., Bagnasco S.;				
RT	"Molecular cloning and functional characterization of a GABA/betaine transporter from human kidney.";				
RT	FEBS Lett. 373:229-233(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Striatum;				
RX	MEDLINE=95165166; PubMed=7861179;				
RA	Borden L.A., Smith K.E., Gustafson E.L., Branchek T.A.,				
RT	Weinstein R.L.;				
RT	"Cloning and expression of a betaine/GABA transporter from human brain.";				
RL	J. Neurochem. 64:977-984(1995).				
CC	- FUNCTION: TRANSPORTS BETAINES AND GABA. MAY HAVE A ROLE IN REGULATION OF GABAERGIC TRANSMISSION IN THE BRAIN THROUGH THE REUPTAKE OF GABA INTO PRESYNAPTIC TERMINALS, AS WELL AS IN OSMOTIC REGULATION.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: LIVER, HEART, SKELETAL MUSCLE, PLACENTA, AND A WIDESPREAD DISTRIBUTION IN THE BRAIN.				
CC	- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER FAMILY (SNF).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: U27699; AAA87029.1; -				
DR	EMBL: LA2300; AAA66574.1; -				
DR	Genew: HGNC:11045; SLC6A12.				
DR	MIM: 603080; -				
DR	InterPro: IPR000175; Na/ntan-symport.				
DR	Pfam: PF00209; SNF; 1.				
DR	PRINTS: PR00176; NAMEUSMPORT.				

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DR PRODOM; PD000448; Na/nturan_symport; 1.
DR PROSITE; PS00610; NA_NEUROTAN_SYM-1; 1.
DR PROSITE; PS00754; NA_NEUROTAN_SYM-2; 1.
DR PROSITE; PS00267; NA_NEUROTAN_SYM-3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 44
FT TRANSMEM 45 65
FT TRANSMEM 73 92
FT TRANSMEM 117 137
FT DOMAIN 138 210
FT TRANSMEM 211 229
FT TRANSMEM 238 255
FT TRANSMEM 291 308
FT TRANSMEM 320 341
FT TRANSMEM 374 393
FT TRANSMEM 423 441
FT TRANSMEM 458 478
FT TRANSMEM 499 518
FT TRANSMEM 538 556
FT DOMAIN 557 614
FT CARBOHYD 171 171
FT CARBOHYD 183 183
FT CONFLICT 10 10
FT CONFLICT 571 572
SQ SEQUENCE 614 AA; 69428 MW; EDC508F97D0B3CA CRC64;

Query Match 100.0%; Score 75; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 1; 6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
DB 583 KOHPCLDGSAGRN 595
|||||
ID HIS6_LISIN STANDARD; PRT; 251 AA.
AC 092E88;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hisF) (Imgp synthase
DE subunit hisF) (IGPS subunit hisF).
GN HISF OR LIND0572.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_Taxid=1642;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Chablit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domani E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entlan K.-D., Esht H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
RA Madueno E., Maitournem A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
[1]
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
-1- FUNCTION: IGP synthase catalyzes the conversion of PRFAR and glutamine to
IGP, AICAR and glutamate. The hisF subunit catalyzes the
cyclization activity that produces IGP and AICAR from PRFAR using
the ammonia provided by the hisH subunit (By similarity).
-1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
ylamino)methylideneamino]-1-[(5-phosphoribosyl)imidazole-4-

```

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CC carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
CC aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
-1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HISF / HISF FAMILY.
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CC or send an email to license@sdb-sdb.ch).
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DR EMBL; AL596165; CAC95804.1; -.
DR EST; L1N00572; -.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000570; His_biosynth.
DR InterPro; IPR001468; IGPS.
DR Pfam; PF00977; His_biosynth; 1.
DR Pfam; PF00218; IGPS; 1.
DR TIGR; TIGR00735; hisF; 1.
KW Histidine biosynthesis; Lyase; Complete proteome.
FT ACT_SITE 11 11
FT ACT_SITE 130 130
FT ACT_SITE 130 130
SQ SEQUENCE 251 AA; 26670 MW; F7C08CDEA909170 CRC64;

Query Match 52.0%; Score 39; DB 1; Length 251;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PCLDGSAGR 12
DB 8 PCLDVYAGR 16
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ID HIS6_LISMO STANDARD; PRT; 251 AA.
AC 08Y9G5;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hisF) (Imgp synthase
DE subunit hisF) (IGPS subunit hisF).
GN HISF OR LMO0563.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_Taxid=1639;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-EGD- / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Chablit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domani E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entlan K.-D., Esht H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
RA Madueno E., Maitournem A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
[1]
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
-1- FUNCTION: IGP synthase catalyzes the conversion of PRFAR and glutamine to
IGP, AICAR and glutamate. The hisF subunit catalyzes the
cyclization activity that produces IGP and AICAR from PRFAR using
the ammonia provided by the hisH subunit (By similarity).
-1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-

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CC      ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC      carboxamide + L-glutamine - imidazole-glycerol phosphate + 5-
CC      aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC      -1- PATHWAY: Histidine biosynthesis; fifth step.
CC      -1- SUBUNIT: Heterodimer of hisH and hisF (by similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC      -1- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      DR      EMBL; AL591975; CAC98642.1; -.
CC      DR      LISTLIST; LMO00563; -.
CC      DR      TIGRFBMS; TIGR00735; hisF; 1.
CC      DR      W      Histidine biosynthesis; Lyase; Complete proteome.
CC      FT      ACT_SITE 11 11 POTENTIAL.
CC      FT      ACT_SITE 130 130 POTENTIAL.
CC      SQ      SEQUENCE 251 AA; 26532 MW; AFE142080F39C67D CRC64;

Query Match          52.0%; Score 39; DB 1; Length 251;
Best Local Similarity 77.8%; Pred. NO. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 PCLDGSAGR 12
        |||||
        8 PCLDVTAGR 16

DB

RESULT 4
HIS6__SYNY3          STANDARD:          PRT: 261 AA.
ID      HIS6__SYNY3
AC      P74106;
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (ICP
DE      synthase cyclase subunit) (ICP synthase subunit hisF) (ImGP synthase
DE      subunit hisF) (IGPS subunit hisF).
DE      GN      SLI1893.
OS      Synechocystis sp. (strain PCC 6803).
OC      Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX      NCBI_TaxID=1148;
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 FT DISULFID 127 142 BY SIMILARITY.
 FT DISULFID 147 157 BY SIMILARITY.

Query Match Best Local Similarity 52.0%; Score 39; DB 1; Length 4660;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOHPLDGSAGR 13
 Db 1088 RONDCLDGSDEON 1100

RESULT 6

SAKL_CHICK STANDARD; PRT; 232 AA.
 ID SAKL_CHICK
 AC P19601;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein SAK-1 (CHOX-3) (Fragment).
 GN SAK1 OR CHOX-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 NC NCBF_TaxID=9031;
 RN [1]
 RP MEDLINE=8930660; PubMed=2568317;
 RA Rangin Z., Fumkin A., Shani G., Guttman M., Eyal-Giladi H.,
 RA Gruenbaum Y., Fainsod A.,
 RT "The chicken homeo box genes Chox1 and Chox3: cloning, sequencing and
 RT expression during embryogenesis.";
 RL Gene 76:61-74(1989).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: TRANSLATIONALLY EXPRESSED IN THE BIRTH ZONE OF THE
 CC WHOLE SPINAL CORD REGARDLESS OF THE AXIAL LEVEL.
 CC -1- SIMILARITY: BELONGS TO THE NK-1 HOMEBOX FAMILY.

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 CC or send an email to license@sib-sib.ch).

CC EMBL: M23065; AAA48821.1; -
 CC PIR: J00069; J00069.
 DR HSP: P14653; I872.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox.1.
 DR ProDom: PD000010; Homeobox.1.
 DR SMART: SM00389; HOX.1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DOMAIN 54 57 POLY-ARG.
 FT DNA_BIND 65 124 HOMEBOX.
 SQ SEQUENCE 232 AA: 25223 MW: 732684E381555C1 CRC64;

Query Match Best Local Similarity 50.7%; Score 38; DB 1; Length 232;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KOHPLDGS 10
 Db 122 KOHPLDGS 131

RESULT 7

IBP4_SHEEP STANDARD; PRT; 237 AA.
 ID IBP4_SHEEP
 AC Q28893;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
 DE (IGF-binding protein 4).
 GN IGFBP4.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 NC NCBF_TaxID=9940;
 RN [1]
 RP MEDLINE=95151165; PubMed=7531449;
 RA Carr J.M., Grant P.A., Francis G.L., Owens J.A., Wallace J.C.,
 RA Walton P.E.;
 RT "Isolation and characterization of ovine IGFBP-4: protein
 RT purification and cDNA sequence.";
 RL J. Mol. Endocrinol. 13:219-236(1994).

CC -1- FUNCTION: IGF-BINDING PROTEIN Prolong the half-life of the IGFs
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY.

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 CC or send an email to license@sib-sib.ch).

CC EMBL: S77394; AB33382.1; -
 CC HSP: P24593; I80E.
 DR InterPro: IPR000867; InsL-grf_fac_pr.
 DR InterPro: IPR000716; Thyroglobulin_1.
 DR Pfam: PF00086; thyroglobulin_1; 1.
 DR Pfam: PF00129; IGFBP.1.
 DR SMART: SM00121; IB; 1.
 DR SMART: SM00211; TY; 1.
 DR PROSITE: PS00222; IGF_BINDING.1.
 DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
 KW Growth factor binding; Glycoprotein.
 FT DOMAIN 179 228 THYROGLOBULIN TYPE I.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 237 AA: 25869 MW: EBC80D4C7667A226 CRC64;

Query Match Best Local Similarity 50.7%; Score 38; DB 1; Length 237;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSAGR 12
 Db 195 HPCLDGSAGR 204

RESULT 8

IBP4_MOUSE

ID IBP4_MOUSE STANDARD: PRT; 254 AA.
AC P47879; 035666; (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Insulin-like growth factor binding protein 4 precursor (IGFBP-4)
DE (IBP-4) (IGF-binding protein 4).
GN IGFBP4 OR IGFBP-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE: Liver;
RX MEDLINE:95121750; PubMed:7529732;
RA Schuller A.G.P., Groffen C., van Neck J.W., Zwartthoff E.C.,
RT DROPP S.L.S.;
RT "cDNA cloning and mRNA expression of the six mouse Insulin-like
RT growth factor binding proteins.";
RT Mol. Cell. Endocrinol. 104:57-66(1994).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN:G57BL/6J;
RX MEDLINE:95152444; PubMed:7531538;
RA Bethel C.R., Vitullo J.C., Miller R.E., Aron D.C.;
RT "Molecular cloning of mouse Insulin-like growth factor binding
RT protein 4 (IGFBP4) cDNA and expression of a fusion protein with
RT IGF-binding activity.";
RT Biochem. Mol. Biol. Int. 34:385-392(1994).
RN (3)
RP SEQUENCE OF 1-114 FROM N.A.
RC STRAIN:BA1B/C; TISSUE:Brain;
RX MEDLINE:98127740; PubMed:9468222;
RA Glanzenberg H., Varga F., Luegmayer E., Klaushofer K.;
RT "Characterization of the mouse Insulin-like growth factor binding
RT protein 4 gene regulatory region and expression studies.";
RT DNA Cell Biol. 17:51-60(1998).
RN (1)
RP FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: BINDS IGF-II MORE THAN IGF-I.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X81582; CAAS7272.1; -;
DR EMBL: X76066; CAAS3667.1; -;
DR EMBL: Z95492; CAB08859.1; -;
DR HSSP: P24593; IBOE.
DR MGD: MGT:96439; Igfbp4.
DR InterPro: IPR000867; Insl_gro_fac_dr.
DR InterPro: IPR000716; Thyroglobulin_1.
DR Pfam: PF00086; thyroglobulin_1; 1.
DR SMART: SM00121; IB: 1.
DR SMART: SM00211; TY: 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
KW Growth factor binding; Signal; Glycoprotein.
FT STGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 254 INSULIN-LIKE GROWTH FACTOR BINDING
FT PROTEIN 4.

FT DOMAIN 196 245 THYROGLOBULIN TYPE I.
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 5 FG -> CS (IN REF. 1).
FT CONFLICT 13 13 A -> T (IN REF. 1).
FT CONFLICT 56 56 C -> S (IN REF. 1).
FT CONFLICT 67 67 C -> G (IN REF. 1).
SQ SEQUENCE 254 AA; 27807 MW; 58EF89CB514AE517 CRC64;
Query Match 50.7%; Score 38; DB 1; Length 254;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 3 HPCLDGSAGR 12
Db 212 HPALDGGGRK 221
RESULT 9
ID IBP4_RAT STANDARD: PRT; 254 AA.
AC P21744;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Insulin-like growth factor binding protein 4 precursor (IGFBP-4)
DE (IBP-4) (IGF-binding protein 4).
GN IGFBP4 OR IGFBP-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE:91133415; PubMed:1704481;
RA Shimasaki S., Uchiyama F., Shimasaka M., Ling N.;
RT "Molecular cloning of the cDNAs encoding a novel Insulin-like growth
RT factor-binding protein from rat and human.";
RT Mol. Endocrinol. 4:1451-1458(1990).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN:Sprague-Dawley;
RX MEDLINE:93176147; PubMed:7679899;
RA Gao L., Ling N., Shimasaki S.;
RT "Structure of the rat Insulin-like growth factor binding protein-4
RT gene.";
RT Biochem. Biophys. Res. Commun. 190:1053-1059(1993).
RN (3)
RP SEQUENCE OF 22-61.
RC TISSUE:Serum;
RX MEDLINE:90073708; PubMed:2480123;
RA Shimomura M., Schroeder R., Shimasaki S., Ling N.;
RT "Identification of a novel binding protein for Insulin-like growth
RT factors in adult rat serum.";
RT Biochem. Biophys. Res. Commun. 165:189-195(1989).
RN (1)
RP FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: BINDS IGF-II MORE THAN IGF-I.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL: L08276; -; NOT_ANNOTATED_CDS.

DR PIR: B33570; B33570.
 DR InterPro: IP000867; Ins1_gro_fac-pr.
 DR PIR: A37252; A37252.
 DR PIR: JCI464; JCI464.
 DR PIR: E40403; E40403.
 DR HSP: P24593; IBOE.
 DR InterPro: IP000867; Ins1_gro_fac-pr.
 DR InterPro: IP000716; Thyroglobulin_1.
 DR Pfam: PF00086; Thyroglobulin_1.
 DR Pfam: PF00219; IGFBP_1.
 DR SMART: SM00121; IB; 1.
 DR SMART: SM00211; TY; 1.
 DR PROSITE: PS00222; IGF-BINDING; 1.
 DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
 DR Growth factor binding: Signal; Glycoprotein.
 FT SIGNAL 1 21
 FT CHAIN 22 254
 FT CARBOHYD 125 125
 FT DOMAIN 196 245
 FT SEQUENCE 254 AA; 27745 MW; 97D37AC98BD0E787 CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 THYROGLOBULIN TYPE I.
 Query Match 50.7%; Score 38; DB 1; Length 254;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSGR 12
 DB 212 HPALDQGRK 221

RESULT 10
 IBP4_BOVIN STANDARD; PRT; 258 AA.
 ID IBP4_BOVIN STANDARD; PRT; 258 AA.
 AC Q05716;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Insulin-like growth factor binding protein 4 precursor (IGFBP-4)
 DE (IBP-4) (IGF-binding protein 4).
 GN IGFBP4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93125553; PubMed-1282670;
 RA Moser D.R., Lowe W.L. Jr., Dake B.L., Booth B.A., Boes M.,
 RA Clemmons D.R., Bar R.S.;
 RA "Endothelial cells express insulin-like growth factor-binding
 RT proteins 2 to 6".
 RT Mol. Endocrinol. 6:1805-1814(1992).
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: BINDS IGF-II MORE THAN IGF-I.
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: S52770; AAB24873.1; -
 CC PIR: A45403; A45403.

DR HSP: P24593; IBOE.
 DR InterPro: IP000867; Ins1_gro_fac-pr.
 DR InterPro: IP000716; Thyroglobulin_1.
 DR Pfam: PF00086; Thyroglobulin_1.
 DR Pfam: PF00219; IGFBP_1.
 DR SMART: SM00121; IB; 1.
 DR SMART: SM00211; TY; 1.
 DR PROSITE: PS00222; IGF-BINDING; 1.
 DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
 DR Growth factor binding: Signal; Glycoprotein.
 FT SIGNAL 1 21
 FT CHAIN 22 258
 FT CARBOHYD 125 125
 FT DOMAIN 200 249
 FT SEQUENCE 258 AA; 27890 MW; A9FDB63B52F0AEF1 CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 THYROGLOBULIN TYPE I.
 Query Match 50.7%; Score 38; DB 1; Length 258;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSGR 12
 DB 216 HPALDQGRK 225

RESULT 11
 IBP4_HUMAN STANDARD; PRT; 258 AA.
 ID IBP4_HUMAN STANDARD; PRT; 258 AA.
 AC P2692;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Insulin-like growth factor binding protein 4 precursor (IGFBP-4)
 DE (IBP-4) (IGF-binding protein 4).
 GN IGFBP4 OR IBP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-91186988; PubMed-1707125;
 RA Latour D., Mohan S., Linkhart T.A., Baylink D.J., Strong D.D.;
 RA "Inhibitory Insulin-like growth factor-binding protein: cloning,
 RT complete sequence, and physiological regulation.";
 RT Mol. Endocrinol. 4:1806-1814(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Placenta;
 RA MEDLINE-91133415; PubMed-1704481;
 RA Shimasaki S., Uchiyama F., Shimonaka M., Ling N.;
 RA "Molecular cloning of the cDNAs encoding a novel insulin-like growth
 RT factor-binding protein from rat and human.";
 RT Mol. Endocrinol. 4:1451-1458(1990).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-41.
 RA TISSUE-Osteosarcoma;
 RA MEDLINE-91325006; PubMed-1709161;
 RA Kiefer M.C., Maslarsz F.R., Bauer D.M., Zapf J.;
 RA "Identification and molecular cloning of two new 30-kDa insulin-like
 RT growth factor binding proteins isolated from adult human serum.";
 RT J. Biol. Chem. 266:9043-9049(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Placenta;
 RA Strong D.D., Morales S., Lee K., Boonyaratankornkit V.,
 RA Baylink D.J., Mohan S.;
 RA Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Colon;
 RA Strausberg R.

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 22-53.
 RC TISSUE:Colon;
 RX MEDLINE:91235178; PubMed-1709585;
 RA Culouscou J.-M., Shoyab M.;
 RT "Purification of a colon cancer cell growth inhibitor and its
 identification as an insulin-like growth factor binding protein.";
 RL Cancer Res. 51:2813-2819(1991).
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
 AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
 INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BINDS IGF-II MORE THAN IGF-I.
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: M38177; NOT_ANNOTATED_CDS.
 CC EMBL: M62403; AAB06189.1; -
 CC EMBL: U20982; AAB62670.1; -
 CC EMBL: BC016041; AAB16041.1; -
 CC PIR: A36549; A36549.
 CC PIR: B37252; B37252.
 CC PIR: B39842; B39842.
 CC HSSP: P24593; IBOE.
 CC Genew: HGNC:5473; IGFBP4.
 CC MIM: 146733; -
 CC InterPro: IPR000867; InsL_gro_fac-Pr.
 CC InterPro: IPR00716; Thyroglobulin_1.
 CC Pfam: PF00086; thyroglobulin_1; 1.
 CC Pfam: PF00219; IGFBP; 1.
 CC SMART: SM00211; IB; 1.
 CC SMART: SM00211; TY; 1.
 CC PROSITE: PS00222; IGF_BINDING; 1.
 CC PROSITE: PS00484; THYROGLOBULIN_1; 1.
 CC Growth factor binding; Signal; Glycoprotein; Polymorphism.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 258
 CC FT CARBOHYD 125 125
 CC FT DOMAIN 200 249
 CC FT VARIANT 42 42
 CC FT VARIANT V -> G (IN DBSNP:599199).
 CC FT VARIANT /FTID-VAR-011906.
 CC FT CONFLICT 51 51 P -> A (IN REF. 1, 4 AND 6).
 CC FT CONFLICT 198 198 I -> F (IN REF. 1 AND 4).
 CC FT SEQUENCE 258 AA; 27934 MW; 5E8F4638D99F0A94 CRC64;
 SQ
 Query Match 50.7%; Score 38; DB 1; Length 258;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 HPCLDGSAGR 12
 DB 216 HPALDGGGRK 225
 RESULT 12
 HIS6_ANASP STANDARD; PRT; 259 AA.
 ID HIS6_ANASP
 AC 08Y131;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Imidazole glycerol phosphate synthase subunit hlsf (EC 4.1.3.-) (IGP
 DE synthase cyclase subunit) (IGP synthase subunit hlsf) (Imge synthase
 DE subunit hlsf) (IGPs subunit hlsf).
 GN Hlsf OR ALR2895.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID:103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:21595285; PubMed-11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Katsube A., Irliguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpso S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
 IGP, AICAR and glutamate. The hlsf subunit catalyzes the
 cyclization activity that produces IGP and AICAR from PRFAR using
 the ammonia provided by the hlsf subunit (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 ylamino)methyl]diphenylamino-1-[(5-phosphoribosyl)imidazole-4-
 carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
 aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hlsf and hlsf (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE HISA / Hlsf FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP003591; BAB74594.1; -
 CC DR TIGRFAMs: TIGR00735; hlsf; 1.
 CC KW Histidine biosynthesis; Lyase; Complete proteome.
 CC FT ACT_SITE 11 11
 CC FT ACT_SITE 130 130 POTENTIAL.
 CC FT SEQUENCE 259 AA; 27918 MW; 9C7BEAA72BFB005E CRC64;
 SQ
 Query Match 50.7%; Score 38; DB 1; Length 259;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 PCLDVKSAGR 12
 DB 8 PCLDVKSAGR 16
 RESULT 13
 YX11_CAEL STANDARD; PRT; 471 AA.
 ID YX11_CAEL
 AC Q11122;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 54.3 kDa protein C03F11.1 in chromosome X.
 GN C03F11.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID:6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bentley D.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -----
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CC -----
CC EMBL: U39744; AAK18882.1; -
CC Morneped: C03F11.1; CE03913.
CC InterPro: IPR004178; CAMD.
CC InterPro: IPR001622; K-channel_pore.
CC InterPro: IPR003931; SK_channel.
CC Pfam: PF02888; CAMD; 1.
CC Hypothetical protein: Transmembrane.
CC Pfam: PF03530; SK_channel; 1.
CC TRANSMEM 78 98 POTENTIAL.
CC TRANSMEM 121 141 POTENTIAL.
CC TRANSMEM 157 177 POTENTIAL.
CC TRANSMEM 263 283 POTENTIAL.
CC TRANSMEM 328 348 POTENTIAL.
CC SEQUENCE 471 AA; 54338 MW; C38F384125A3A830 CRC64;
SQ
Query Match 50.7%; Score 38; DB 1; Length 471;
Best Local Similarity 63.68; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3 HPCLDGSAGR 13
Db 389 HKCLOGSDCGN 399
RESULT 14
ID RGPL_XENLA STANDARD; PRT; 580 AA.
AC 013066;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ran-GTPase activating protein 1.
GN RANGAP1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8335;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=97268639; PubMed=9108047;
RA Satoh H., Pu R., Cavenagh M., Dasso M.;
RT "RanBP2 associates with ubp9 C, and a modified form of RANGAP1."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3736-3741(1997).
CC -1- FUNCTION: GTPASE ACTIVATOR FOR THE NUCLEAR RAS-RELATED REGULATORY
CC PROTEIN RAN, CONVERTING IT TO THE PUTATIVELY INACTIVE GDP-BOUND
CC STATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER. FORMS A TIGHT COMPLEX IN ASSOCIATION WITH
CC RANBP2 AND THE UBIQUITIN-CONJUGATING ENZYME E2 (UBC9).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- PM: SEEMS TO BE CONVERTED TO A 20 kDa HEAVIER FORM BY CONJUGATION
CC WITH A SMALL UBIQUITIN-LIKE PROTEIN UBL1 (SUMO-1).
CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: TO FUNGAL RNL.
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CC -----

CC EMBL: U88155; AAB62321.1; -
CC DR HSP7_YEAST
CC DR InterPro: IPR003592; LRR_out.
CC DR SMART: SM00370; LRR; 7.
CC KW GTPase activation; Repeat; Leucine-rich repeat; Ubl conjugation.
CC FT REPEAT 48 71 LRR 1.
CC FT REPEAT 111 134 LRR 2.
CC FT REPEAT 141 168 LRR 3.
CC FT REPEAT 207 230 LRR 4.
CC FT REPEAT 235 258 LRR 5.
CC FT REPEAT 292 315 LRR 6.
CC FT REPEAT 320 343 LRR 7.
CC FT DOMAIN 359 396 ASP/GLU-RICH (HIGHLY ACIDIC).
CC SEQUENCE 580 AA; 62907 MW; BE1ED7693E8FE3E CRC64;
SQ
Query Match 50.7%; Score 38; DB 1; Length 580;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KOHCLDGS 10
Db 407 KEIPCLDGS 416
RESULT 15
HSP7_YEAST
ID HSP7_YEAST STANDARD; PRT; 811 AA.
AC P33416;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock protein 78, mitochondrial precursor.
GN HSP78 OR YDR258C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94019304; PubMed=8413229;
RA Leonhardt S.A., Fearon K., Danese P.N., Mason T.L.;
RT "HSP78 encodes a yeast mitochondrial heat shock protein in the Clp
RT family of ATP-dependent proteases."
RL Mol. Cell. Biol. 13:6304-6313(1993).
[2]
RN FUNCTION.
RP MEDLINE=95354661; PubMed=7628444;
RX Schmitt M., Neupert W., Langer T.;
RA "Hsp78, a Clp homologue within mitochondria, can substitute for
RT chaperone functions of mt-hsp70."
RL EMBL J. 14:3434-3444(1995).
CC -1- FUNCTION: SEEMS TO BE INVOLVED IN THE TURNOVER OF UNASSEMBLED
CC MITOCHONDRIAL PROTEINS.
CC -1- SUBUNIT: POSSIBLY PART OF AN ATP-DEPENDENT PROTEASE.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- INDUCTION: BY HEAT SHOCK AND CARBON SOURCE.
CC -1- SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
CC -----
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CC -----
CC EMBL: L16533; AAC37362.1; -
CC PIR: S39001; S39001.
CC SGD: S0002666; HSP78.
CC InterPro: IPR003593; AAA_ATPase.
CC InterPro: IPR003959; AAA_ATPase_cent.
CC InterPro: IPR001270; Chaprinin_ClpA/B.
CC -----

DR Pfam; PF00004; AAA; 1.
DR PRINTS; PR00300; CLPEPTASEA.
DR PRODOM; PD000739; GSEPI_E; 1.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00870; CLPAB_1; 1.
DR PROSITE; PS00871; CLPAB_2; 1.
KW Chaperone; ATP-binding; Repeat; Heat shock; Mitochondrion;
KW Transil peptide.
FT TRANSIT 1 53 MITOCHONDRION (POTENTIAL).
FT CHAIN 54 811 HEAT SHOCK PROTEIN 78.
FT DOMAIN 98 344 I (BY SIMILARITY).
FT DOMAIN 467 658 IT (BY SIMILARITY).
FT NP_BIND 143 150 ATP (POTENTIAL).
FT NP_BIND 541 548 ATP (POTENTIAL).
SQ SEQUENCE 811 AA; 91287 MW; EA9437C5F5610867 CRC64;

Query Match 50.7%; Score 38; DB 1; Length 811;
Best Local Similarity 63.6%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 KOHPCLDGSAG 11
136 KNNPCLIGRAG 146

Search completed: February 21, 2003, 16:11:49
Job time : 20.4194 secs

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OM protein - protein search, using sw model

Run on: February 21, 2003, 16:03:01 : Search time 36.5806 Seconds

(Without alignments)
65.568 Million cell updates/sec

Title: US-09-992-067-1

Perfect score: 91
Sequence: 1 KSPEDQETVLGDLNLTIR 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	339	22	AAU32845
2	91	100.0	930	23	ABR09708
3	91	100.0	930	23	ABR09709
4	86	94.5	123	22	ABR09711
5	86	94.5	921	22	ABR09711
6	79	86.8	16	22	ABR09711
7	57	62.6	932	23	ABR09706
8	57	62.6	933	23	ABR09707
9	46	50.5	179	23	ABP25414
10	46	50.5	179	23	ABP29767

11	45	49.5	452	23	ABR92562
12	44	48.4	409	14	AAE1227
13	43	47.3	650	21	AAE85180
14	43	47.3	858	21	ABP27072
15	43	47.3	946	21	AAE29100
16	42	46.2	419	18	AAE10977
17	42	46.2	419	18	AAE11865
18	42	46.2	544	18	AAE10975
19	42	46.2	544	18	AAE11863
20	42	46.2	544	18	AAE14735
21	42	46.2	544	22	AAE11757
22	42	46.2	544	23	ABR94272
23	42	46.2	652	22	AAE13000
24	42	46.2	652	22	AAE13002
25	42	46.2	704	18	AAE10976
26	42	46.2	704	18	AAE11864
27	42	46.2	858	15	AAE53404
28	42	46.2	858	19	AAE49080
29	42	46.2	2515	22	ABR64427
30	41.5	45.6	346	22	AAE82710
31	41.5	45.6	353	23	ABP99795
32	41	45.1	140	22	AAE10209
33	41	45.1	189	22	AAE18354
34	41	45.1	258	20	AAE37099
35	41	45.1	276	23	ABR48710
36	41	45.1	544	12	AAE13337
37	41	45.1	612	22	AAE34514
38	41	45.1	628	22	ABG24763
39	41	45.1	901	23	AAE66003
40	40.5	44.5	263	23	ABP27541
41	40.5	44.5	434	16	AAE21805
42	40.5	44.5	436	12	AAE14448
43	40.5	44.5	436	13	AAE28495
44	40.5	44.5	436	16	AAE17123
45	40.5	44.5	436	16	AAE21806

ALIGNMENTS

RESULT 1
AAU32845
ID AAU32845 standard; Protein; 339 AA.

AC AAU32845;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #3336.

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

Herbicidally active
910 SLG protein.
Cellulose synthase
Streptococcus poly
Human inter-alpha-
dihydrofolate redu
DHFR/Polypeptide B
Chlamydia pneumonia
Polypeptide B. Ch
Amino acid sequenc
Chlamydia pneumonia
Chlamydia pneumonia
Corn poly (A) bind
Glycine max poly (A)
Dihydrofolate redu
DHFR/Polypeptide B
S-Locus receptor (B)
Brassica sp. S-rec
Drosophila melanog
S. epidermidis ope
Staphylococcus epi
Human bone marrow
Human endocrine po
Amino acid sequenc
Listeria monocytog
Hyp protein. Chl
E. coli cellular p
Novel human diagno
P. patens cell cyc
Streptococcus poly
Spliced-deleted in
Soluble interferon
Sequence of a soul
IFN receptor extra
Spliced-deleted in

XX Claim 20; Page 678; 765pp; English.
PS The invention relates to novel human secreted polypeptides. The
PS polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
Sequence 339 AA:
Query Match 100.0%; Score 91; DB 22; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KSPQEQETVLDGNLIIRY 18
DB 124 KSPQEQETVLDGNLIIRY 141
|||||
RESULT 2
ABB09708 ABB09708 standard; Protein; 930 AA.
XX
AC ABB09708;
XX
DT 11-JUN-2002 (first entry)
XX
DE Sequence of H4P heavy chain of Inter alpha trypsin inhibitor.
XX
KM MAY-1; blood transfusion; immunosuppressive; mixed lymphocyte reaction;
KM MLR; autoimmune disease; allergic disease; organ rejection;
KM organ transplantation; rheumatism; psoriasis; bronchial asthma;
KM allergic rhinitis; allergic dermatitis; pollinosis; H4P heavy chain;
KM Inter alpha trypsin inhibitor.
XX
OS Homo sapiens.
XX
PD WO200212495-A1.
XX
PD 14-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-JP06620.
XX
PR 09-AUG-2000; 2000JP-0241169.
XX
PA (MARU-) MARUHO KK.
XX
PI Uchida H, Tanaka H, Kitch Y, Fujimura A, Kobayashi E;
XX
DR WPI: 2002-217191/27.
DR N-PSDB; ABL41971.
XX
PT Rat or human protein MAY-1 induced by homogeneous blood transfusion and
PT exhibiting immunosuppressive activity in a homogeneous mixed lymphocyte
PT reaction, for providing drug compositions to treat e.g. autoimmune
PT diseases -
XX
PS Disclosure: Page 55-59; 85pp; Japanese.
XX
CC The present sequence represents the human H4P heavy chain of Inter

CC alpha trypsin inhibitor protein. The specification describes MAY-1
CC protein, which is induced by homogeneous blood transfusion. MAY-1
CC exhibits an immunosuppressive activity in a homogeneous mixed
CC lymphocyte reaction (MLR). The MAY-1 protein can formulated into drug
CC compositions for the prevention or treatment of autoimmune diseases,
CC allergic diseases, or rejection reaction during organ transplantation,
CC e.g. rheumatism, psoriasis, bronchial asthma, allergic rhinitis,
CC allergic dermatitis and pollinosis.
XX
SQ Sequence 930 AA;
Query Match 100.0%; Score 91; DB 23; Length 930;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KSPQEQETVLDGNLIIRY 18
DB 224 KSPQEQETVLDGNLIIRY 241
|||||
RESULT 3
ABB09709 ABB09709 standard; Protein; 930 AA.
XX
AC ABB09709;
XX
DT 11-JUN-2002 (first entry)
XX
DE Amino acid sequence of a human PK-120 polypeptide.
XX
KM MAY-1; blood transfusion; immunosuppressive; mixed lymphocyte reaction;
KM MLR; autoimmune disease; allergic disease; organ rejection;
KM organ transplantation; rheumatism; psoriasis; bronchial asthma;
KM allergic rhinitis; allergic dermatitis; pollinosis; PK-120; ss.
XX
OS Homo sapiens.
XX
PN WO200212495-A1.
XX
PD 14-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-JP06620.
XX
PR 09-AUG-2000; 2000JP-0241169.
XX
PA (MARU-) MARUHO KK.
XX
PI Uchida H, Tanaka H, Kitch Y, Fujimura A, Kobayashi E;
XX
DR WPI: 2002-217191/27.
DR N-PSDB; ABL41972.
XX
PT Rat or human protein MAY-1 induced by homogeneous blood transfusion and
PT exhibiting immunosuppressive activity in a homogeneous mixed lymphocyte
PT reaction, for providing drug compositions to treat e.g. autoimmune
PT diseases -
XX
PS Disclosure: Page 62-66; 85pp; Japanese.
XX
CC The present sequence represents a human PK-120 polypeptide. The
CC specification describes MAY-1 protein, which is induced by
CC homogeneous blood transfusion. MAY-1 exhibits an immunosuppressive
CC activity in a homogeneous mixed lymphocyte reaction (MLR). The MAY-1
CC protein can formulated into drug compositions for the prevention or
CC treatment of autoimmune diseases, allergic diseases, or rejection
CC reaction during organ transplantation, e.g. rheumatism, psoriasis,
CC bronchial asthma, allergic rhinitis, allergic dermatitis and pollinosis.
XX
SQ Sequence 930 AA;
Query Match 100.0%; Score 91; DB 23; Length 930;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPQOETVLDGNLIIRY 18
 |||||||
 Db 224 KSPQOETVLDGNLIIRY 241

RESULT 4
 ID AAU32844
 AAU32844 standard; Protein: 123 AA.

AC AAU32844;
 DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #3335.

OS Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 MW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HXSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

PS Claim 20; Page 676-678; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 123 AA;

Query Match 94.5%; Score 86; DB 22; Length 123;
 Best Local Similarity 94.4%; Pred. No. 2.7e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSPQOETVLDGNLIIRY 18
 |||||||
 Db 53 KSPQOETVLDGNLIIRY 70

RESULT 5
 ABB09711

ID ABB09711 standard; Protein: 921 AA.

XX ABB09711;

DT 11-JUN-2002 (first entry)

DE Sequence of H4P heavy chain of inter-alpha-inhibitor protein.

KW MAY-1; blood transfusion; immunosuppressive; mixed lymphocyte reaction;
 KW MCR; autoimmune disease; allergic disease; organ rejection;
 KW organ transplantation; rheumatism; psoriasis; bronchial asthma;
 KW allergic rhinitis; allergic dermatitis; pollinosis; H4P heavy chain;
 KW inter-alpha-inhibitor protein.

OS Sps sp.

PN WO200212495-A1.

PD 14-FEB-2002.

PF 01-AUG-2001; 2001WO-JP06620.

PR 09-AUG-2000; 2000JP-0241169.

PA (MARU-) MARUHO KK.

PI Uchida H, Tanaka H, Kitoh Y, Fujimura A, Kobayashi E;

DR WPI: 2002-217191/27.

DR N-PSDB; ABL41975.

PT Rat or human protein MAY-1 induced by homogeneous blood transfusion and
 PT exhibiting immunosuppressive activity in a homogeneous mixed lymphocyte
 PT reaction, for providing drug compositions to treat e.g. autoimmune
 PT diseases -

PS Disclosure; Page 71-75; 85pp; Japanese.

XX The present sequence represents the hog H4P heavy chain of
 CC inter-alpha-inhibitor protein. The specification describes MAY-1
 CC protein, which is induced by homogeneous blood transfusion. MAY-1
 CC exhibits an immunosuppressive activity in a homogeneous mixed
 CC lymphocyte reaction (MLR). The MAY-1 protein can formulated into drug
 CC compositions for the prevention or treatment of autoimmune diseases,
 CC allergic diseases, or rejection reaction during organ transplantation,
 CC e.g. Rheumatism, psoriasis, bronchial asthma, allergic rhinitis,
 CC allergic dermatitis and pollinosis.

XX Sequence 921 AA;

Query Match 94.5%; Score 86; DB 23; Length 921;
 Best Local Similarity 88.9%; Pred. No. 3.3e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSPQOETVLDGNLIIRY 18
 |||||||
 Db 222 KSPQOETVLDGNLIIRY 239

RESULT 6

ID ABB52029 standard; Peptide: 16 AA.

XX ABB52029;

DT 08-FEB-2002 (first entry)

DE Human API-57 tryptic digest peptide #2.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.

```
XX OS Homo sapiens.
XX PN WO200175454-A2.
XX PD 11-OCT-2001.
XX PF 03-APR-2001; 2001WO-US10908.
XX PR 03-APR-2000; 2000US-194504P.
XX PR 28-NOV-2000; 2000US-253647P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA (PFIZ ) PFIZER INC.
XX PI Durham KL, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;
XX PI Potter DM, Rohlf C, Silber BM, Stigler TR, Sunderland PT;
XX PI Townsend RR, White F, Williams SA;
XX DR WPI; 2001-639384/73.
XX PT Screening for Alzheimer's disease in a mammal, by making
XX PT two-dimensional array of a feature whose relative abundance correlates
XX PT with disease, and comparing with abundance of the feature in samples of
XX PT healthy persons.
XX PS Example; Page 26; 162pp; English.
XX CC The invention relates to methods for the screening, diagnosis and
XX CC prognosis of Alzheimer's disease. The methods involve the detection
XX CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
XX CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
XX CC serum or plasma. The abundance of the AFs and APIs is then
XX CC normalised to an Expression Reference Protein Isoform (ERPI) in
XX CC order to determine whether a patient is suffering from, or has
XX CC a predisposition to, Alzheimer's Disease. The relative abundance of
XX CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
XX CC The present sequence is a peptide produced from an API by proteolysis.
XX SQ Sequence 16 AA;
XX
XX Query Match 86.8%; Score 79; DB 22; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 SPEQGETVLDGNLIIR 17
DB 1 SPEQGETVLDGNLIIR 16
XX
XX RESULT 7
XX ABB09706
XX ID ABB09706 standard; Protein; 932 AA.
XX AC ABB09706;
XX
XX 11-JUN-2002 (first entry)
XX
XX Sequence of HAP heavy chain of inter-alpha-inhibitor protein.
XX
XX MAY-1; blood transfusion; immunosuppressive; mixed lymphocyte reaction;
XX KM MLR; autoimmune disease; allergic disease; organ rejection;
XX KM organ transplantation; rheumatism; psoriasis; bronchial asthma;
XX KM allergic rhinitis; allergic dermatitis; pollinosis; HAP heavy chain;
XX KM inter-alpha-inhibitor protein.
XX
XX Rattus sp.
XX OS
XX PN WO200212495-A1.
XX PD 14-FEB-2002.
XX PF 01-AUG-2001; 2001WO-JP06620.
```

```
XX PR 09-AUG-2000; 2000JP-0241169.
XX PA (MARU-) MARUHO KK.
XX PI uchida H, Tanaka H, Kitoh Y, Fujimura A, Kobayashi E;
XX DR WPI; 2002-217191/27.
XX DR N-PSDB; ABL41969.
XX PT Rat or human protein MAY-1 induced by homogeneous blood transfusion and
XX PT exhibiting immunosuppressive activity in a homogeneous mixed lymphocyte
XX PT reaction, for providing drug compositions to treat e.g. autoimmune
XX PT diseases.
XX PS Disclosure; Page 43-47; 85pp; Japanese.
XX CC The present sequence encodes the rat HAP heavy chain of
XX CC inter-alpha-inhibitor protein. The specification describes MAY-1
XX CC protein, which is induced by homogeneous blood transfusion. MAY-1
XX CC exhibits an immunosuppressive activity in a homogeneous mixed
XX CC lymphocyte reaction (MLR). The MAY-1 protein can be formulated into drug
XX CC compositions for the prevention or treatment of autoimmune diseases,
XX CC allergic diseases, or rejection reaction during organ transplantation,
XX CC e.g. rheumatism, psoriasis, bronchial asthma, allergic rhinitis,
XX CC allergic dermatitis and pollinosis.
XX SQ Sequence 932 AA;
XX
XX Query Match 62.6%; Score 57; DB 23; Length 932;
XX Best Local Similarity 55.6%; Pred. No. 0.44;
XX Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 1 KSPEQGETVLDGNLIIR 18
DB 223 KSGNEQDVTVDGDFTVRY 240
XX
XX RESULT 8
XX ABB09707
XX ID ABB09707 standard; Protein; 933 AA.
XX AC ABB09707;
XX
XX 11-JUN-2002 (first entry)
XX
XX Sequence of HAP heavy chain of inter-alpha-inhibitor protein.
XX
XX MAY-1; blood transfusion; immunosuppressive; mixed lymphocyte reaction;
XX KM MLR; autoimmune disease; allergic disease; organ rejection;
XX KM organ transplantation; rheumatism; psoriasis; bronchial asthma;
XX KM allergic rhinitis; allergic dermatitis; pollinosis; HAP heavy chain;
XX KM inter-alpha-inhibitor protein.
XX
XX Rattus sp.
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 96 /note= "Leu encoded by AAA"
XX FT Misc-difference 106 /note= "Tyr encoded by ACT"
XX
XX WO200212495-A1.
XX PD 14-FEB-2002.
XX PF 01-AUG-2001; 2001WO-JP06620.
XX PR 09-AUG-2000; 2000JP-0241169.
XX PA (MARU-) MARUHO KK.
XX PI uchida H, Tanaka H, Kitoh Y, Fujimura A, Kobayashi E;
```

XX WPI: 2002-217191/27.
DR N-PSDB: AB141970.
XX
XX Rat or human protein MAY-1 induced by homogeneous blood transfusion and
XX exhibiting immunosuppressive activity in a homogeneous mixed lymphocyte
XX reaction, for providing drug compositions to treat e.g. autoimmune
XX diseases -
XX
XX Claim 3; Page 49-53; 85pp; Japanese.
XX
XX The present sequence encodes the rat H4P heavy chain of
XX inter-alpha-inhibitor protein. The specification describes MAY-1
XX protein, which is induced by homogeneous blood transfusion. MAY-1
XX exhibits an immunosuppressive activity in a homogeneous mixed
XX lymphocyte reaction (MLR). The MAY-1 protein can formulated into drug
XX compositions for the prevention or treatment of autoimmune diseases,
XX allergic diseases, or rejection reaction during organ transplantation,
XX e.g. rheumatism, psoriasis, bronchial asthma, allergic rhinitis,
XX allergic dermatitis and pollinosis.
XX
XX Sequence 933 AA;
XX
XX
XX Query Match 62.6%; Score 57; DB 23; Length 933;
XX Best Local Similarity 55.6%; Pred. No. 0.44;
XX Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 KSPEDQETVLDGNLIIRY 18
XX || :|||::||
XX Db 224 KSONEDOTVLDGDFTVRY 241
XX
XX
XX RESULT 9
XX ABP25414
XX ID ABP25414 standard; Protein: 179 AA.
XX
XX ABP25414;
XX
XX 02-JUL-2002 (first entry)
XX
XX Streptococcus polypeptide SEQ ID NO 4.
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX Streptococcus agalactiae.
XX
XX WO200234771-A2.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-GB04789.
XX
XX 27-OCT-2000; 2000GB-0026333.
XX 24-NOV-2000; 2000GB-0028727.
XX 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX
XX WPI: 2002-352536/38.
XX N-PSDB: ABN66045.
XX
XX New Streptococcus protein for the treatment or prevention of infection
XX or disease caused by Streptococcus bacteria, such as meningitis, and
XX for detecting a compound that binds to the protein -
XX
XX Claim 1; Page 3154; 4525pp; English.
XX

CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
XX
XX Sequence 179 AA;
XX
XX
XX Query Match 50.5%; Score 46; DB 23; Length 179;
XX Best Local Similarity 52.9%; Pred. No. 5;
XX Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
XX 2 SPEDQETVLDGNLIIRY 18
XX ||| || | | :: ||
XX Db 147 SPENDEKAVADNYVVSRY 163
XX
XX
XX RESULT 10
XX ABP29767
XX ID ABP29767 standard; Protein: 179 AA.
XX
XX ABP29767;
XX
XX 02-JUL-2002 (first entry)
XX
XX Streptococcus polypeptide SEQ ID NO 8710.
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX Streptococcus agalactiae.
XX
XX WO200234771-A2.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-GB04789.
XX
XX 27-OCT-2000; 2000GB-0026333.
XX 24-NOV-2000; 2000GB-0028727.
XX 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX
XX WPI: 2002-352536/38.
XX N-PSDB: ABN70398.
XX
XX New Streptococcus protein for the treatment or prevention of infection
XX or disease caused by Streptococcus bacteria, such as meningitis, and
XX for detecting a compound that binds to the protein -
XX
XX Claim 1; Page 3986; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
CC
XX

SQ Sequence 179 AA;

Query Match 50.5%; Score 46; DB 23; Length 179;

Best Local Similarity 52.9%; Pred. No. 5; Mismatches 6; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

2 SPEQOETVLDGNLIRY 18

DB 147 SPENQEKVADNYVSRV 163

RESULT 11

ABR92562 ID ABR92562 standard; Protein; 452 AA.

XX ABR92562;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1773.

XX Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP09892.

PR 28-AUG-2001; 2001WO-EP09892.

PA (PARB) BAYER AG.

PI Tietjen K, Weidner M;

DR WPI: 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,

PT comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms -

XX Claim 5; SEQ ID NO 1773; 261pp + Sequence Listing: English.

CC The invention relates to identifying target proteins

CC (ABR90790-ABR94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant

CC with nucleic acid or amino acid sequences from non-plant organisms using

CC suitable search parameters, where plant sequences having an E-value

CC greater by a factor of 3 than the E-value of most similar non-plant

CC sequences are selected. The polypeptides or nucleic acids encoding them

CC are useful for identifying modulators. The identified modulators are

Query Match 49.5%; Score 45; DB 23; Length 452;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 KSPEQOETVLDGNLIRY 18
DB 160 KDPKQDKVLEGUHLRY 177

RESULT 12

AAK41227 ID AAK41227 standard; Protein; 409 AA.

XX AAK41227;

DT 15-MAR-1994 (first entry)

DE 910 SLG protein.

XX Self-incompatibility; Brassica napus rapifera;

KW Brassica campestris; vector; S-locus; amplification;

KW 910 allele; A14 allele; SLG: self linked glycoproteins;

OS Brassica campestris.

XX Key Location/Qualifiers

FT Peptide 1..31

FT Protein 32..409

FT Modified-site 48

FT Modified-site 116

FT Modified-site 123

FT Modified-site 264

FT Modified-site 393

PN WO9318149-A.

PD 16-SEP-1993.

PF 29-JUN-1992; 92MO-US04530.

PR 03-MAR-1992; 92US-0847564.

PA (PION-) PIONEER HI-BRED INT INC.

PI Baszczynski C, Fallis L, Goring DR, Rothstein SJ;

DR WPI: 1993-303463/38.

XX N-PSDB: AAQ48746.

XX Isolated cDNA sequences corresp. to self-incompatibility alleles

PT in Brassica campestris and B napus ssp. rapifera - are useful for

PT transferring self-incompatibility phenotype to plant cells and

PT protoplasts

XX Claim 2; Fig 9; 64pp; English.

CC The cDNAs encoding self incompatibility sites of B. napus and

CC B. campestris (AAQ48745-46) correspond to genes encoding S-linked

CC glycoproteins which are associated with the expression of

CC sporophytic self-incompatibility. The cDNAs may be used to

CC transform self-compatible plants, plant cells and plant

CC protoplasts, with the aim of introducing the self-incompatibility

CC phenotype.

XX Sequence 409 AA;

Query Match 48.4%; Score 44; DB 14; Length 409;
Best Local Similarity 44.4%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KSPEQETVLDGNLIIRX 18
: || | : || : || |
Db 130 RSPVVAELANGNFVIRY 147

RESULT 13
AAV85180
ID AAV85180 standard; Protein: 650 AA.
XX
AC AAV85180;
XX
XX 29-JUN-2000 (first entry)
XX
XX Cellulose synthase subunit amino acid sequence.
XX
XX Cellulose synthase; cellulose production; increase yield.
XX
XX Vigna angularis.
XX
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 379
XX FT /label= "Unknown
XX FT /note= "Encoded by GTN"
XX
XX PN JP2000060568-A.
XX
XX PD 29-FEB-2000.
XX
XX PF 26-AUG-1998; 98JP-0239998.
XX
XX PR 26-AUG-1998; 98JP-0239998.
XX
XX PA (MIZU/) MIZUNO K.
XX PA (COTIP) COTI PAPER CO.
XX
XX DR WPI: 2000-342371/30.
XX
XX DR N-PSDB; AAA10595.
XX
XX PT A gene encoding a cellulose synthetic equipment - for the improvement
XX PT in the amount of cellulose synthesised in a plant body
XX
XX PS Claim 1; Page 11-14; 32pp; Japanese.
XX
XX CC This sequence represents the amino acid sequence of a subunit of the
XX CC cellulose synthase complex of *Vigna angularis*. The invention relates to
XX CC subunits of cellulose synthetic equipment, that can be used to increase
XX CC the amount of cellulose synthesised by a plant. The proteins and genes
XX CC encoding them can also be used to improve the properties of the cellulose
XX CC being produced by a plant.
XX
XX SQ Sequence 650 AA;

Query Match 47.3%; Score 43; DB 21; Length 650;
Best Local Similarity 69.2%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 SPEQETVLDGNLI 14
: || | | | : || | | |
Db 563 SPEQORTMLGENL 575

RESULT 14
ABP27072
ID ABP27072 standard; Protein: 858 AA.
XX
XX AC ABP27072;
XX
XX DT 02-JUL-2002 (first entry)

XX
DE Streptococcus polypeptide SEQ ID NO 3320.
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX OS Streptococcus agalactiae.
XX
XX PN M0200234771-A2.
XX
XX PD 02-MAY-2002.
XX
XX PF 29-OCT-2001; 2001MO-GB04789.
XX
XX PR 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.
XX
XX PA (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX
XX PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;
XX PI Tetteijn H;
XX
XX DR WPI: 2002-352536/38.
XX DR N-PSDB; ABN67703.
XX
XX PT New Streptococcus protein for the treatment or prevention of infection
XX PT or disease caused by Streptococcus bacteria, such as meningitis, and
XX PT for detecting a compound that binds to the protein -
XX
XX PS Claim 1; Page 3486; 4525pp; English.
XX
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC used as a vaccine or diagnostic composition. The disease caused by
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins.
XX
XX SQ Sequence 858 AA;

Query Match 47.3%; Score 43; DB 23; Length 858;
Best Local Similarity 50.0%; Pred. No. 1.2e+00; Indels 0; Gaps 0;
Matches 7; Conservative 4; Mismatches 3;

QY 2 SPEQETVLDGNLI 15
: || | | | : || | | |
Db 400 APEAQTTEGNI 413

RESULT 15
AAB29100
ID AAB29100 standard; Protein: 946 AA.
XX
XX AC AAB29100;
XX
XX DT 07-FEB-2001 (first entry)
XX
XX DE Human inter-alpha-trypsin inhibitor heavy-chain II precursor.

KW Human; Inter-alpha-trypsin inhibitor heavy-chain II precursor;
 KW cell migration; inflammation; autoimmune disease; fuge-lactic agent.
 XX
 OS Homo sapiens.
 XX
 PN WO200059941-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-US09678.
 XX
 PR 08-APR-1999; 99US-0128272.
 PR 03-DEC-1999; 99US-0168952.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX
 PI Poznansky MC, Luster AD, Scadden DT;
 XX
 DR WPI; 2000-672621/65.
 XX
 PT Isolates from thymic stromal-cell, HepG2-cell or Kaposi's sarcoma
 PT Herpes virus infected-cell useful for treating tumour, infertility and
 PT premature labour, repel immune cells -
 XX
 PS Claim 111; Page 83-85; 87pp; English.
 XX
 CC The present invention is related to the modulation of movement of
 CC eukaryotic cells. This involves the use of fuge-lactic agents, such as the
 CC one shown here. These can be used in the treatment of inflammation and
 CC autoimmune diseases, including rheumatoid arthritis, uveitis, diabetes,
 CC haemolytic anaemias, rheumatic fever, Crohn's disease, Guillain-Barre
 CC syndrome, psoriasis, thyroiditis, Graves' disease, myasthenia gravis,
 CC glomerulonephritis, autoimmune hepatitis and systemic lupus
 CC erythematosus. They can also be used to treat cancer, infertility and
 CC premature labour.
 XX
 SQ Sequence 946 AA;

Query Match 47.3%; Score 43; DB 21; Length 946;
 Best local Similarity 43.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 PEOQETVLDGNLIIRY 18
 I : I I : I I I : I
 Db 262 PSCRETAVDGEIVLVLY 277

Search completed: February 21, 2003, 16:10:58
 Job time : 39.5806 secs

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OW protein - protein search, using sw model

Run on: February 21, 2003, 16:03:01 : Search time 26.4194 Seconds
(without alignments)
65.568 Million cell updates/sec

Title: US-09-992-067-2
Perfect score: 75
Sequence: 1 K0HPCLDGSAGRN 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	100.0	614	15	AAR55799	Human betaine-GABA
2	75	100.0	614	17	AAR89461	Human betaine/GABA
3	75	100.0	1923	22	ABG21342	Novel human diagno
4	47	62.7	88	22	AAU51999	Protonibacterium
5	47	62.0	374	21	AA18979	Amino acid sequenc
6	42	56.0	4601	22	ABBS9371	Drosophila melanog
7	41	54.7	149	22	ABG08064	Novel human diagno
8	41	54.7	174	22	AAU46916	Protonibacterium
9	41	54.7	319	22	ABBS2080	Drosophila melanog
10	40.5	54.0	232	21	AA604837	Arabidopsis thalia

11	40.5	54.0	262	21	AA604836	Arabidopsis thalia
12	40.5	54.0	329	21	AA604835	Arabidopsis thalia
13	40	53.3	72	22	AB15976	Human nervous syst
14	40	53.3	125	22	AA187341	Human immune/haema
15	40	53.3	356	22	AAU42630	Protonibacterium
16	39	52.0	53	21	AA603682	Human secreted pro
17	39	52.0	68	22	AAU40527	Protonibacterium
18	39	52.0	72	22	AAU45133	Protonibacterium
19	39	52.0	80	22	AAU64896	Protonibacterium
20	39	52.0	197	21	AA12159	Human ORFX ORF1923
21	39	52.0	251	23	AB148751	Listeria monocytog
22	39	52.0	254	22	AAU17241	Novel signal trans
23	39	52.0	260	22	AAU87198	Novel central nerv
24	39	52.0	312	22	AAU14605	Novel bone marrow
25	39	52.0	445	23	AB191957	Herbicidially activ
26	39	52.0	598	21	AA620654	Arabidopsis thalia
27	39	52.0	599	21	AA620653	Herbicidially activ
28	39	52.0	751	23	AB193984	Human insulin-resp
29	39	52.0	1028	22	AA1882249	Human insulin-like growt
30	38	50.7	10	20	AA125488	Insulin-like growt
31	38	50.7	14	21	AA166801	T cell antigen rec
32	38	50.7	52	23	AB105976	Human ORFX protein
33	38	50.7	54	21	AA109676	IGFBP-4 IGF bindin
34	38	50.7	79	22	AA184070	Human immune/haema
35	38	50.7	102	20	AA125507	Insulin-like growt
36	38	50.7	123	21	AA158228	Lung cancer associ
37	38	50.7	154	18	AA109068	Banana bunchy top
38	38	50.7	154	18	AA109072	Banana bunchy top
39	38	50.7	159	22	AB127384	Novel human diagno
40	38	50.7	181	22	AAU27529	Human G-Protein Co
41	38	50.7	206	22	AB103882	Novel human diagno
42	38	50.7	233	21	AA109755	IGFBP-4 amino acid
43	38	50.7	233	21	AA167291	Rat insulin-like g
44	38	50.7	236	13	AA121834	Sequence of insuli
45	38	50.7	237	21	AA109620	Insulin like growt

ALIGNMENTS

RESULT 1	AA155799	standard: Protein: 614 AA.
XX	AA155799;	
AC	21-MAY-1998 (first entry)	
XX		
DT	Human betaine-GABA transporter.	
XX		
DE		
XX		
KW	Gamma-aminobutyric acid; GABA; betaine; transporter; detection;	
KW	treatment; epilepsy; migraine; ischaemia; myoclonus; spasticity;	
KW	chronic pain; osmolyte; GABAergic transmission; nervous system;	
KW	osmolarity.	
XX		
OS	Homo sapiens.	
XX		
PN	MO9415618-A.	
XX		
PD	21-JUL-1994	
XX		
PF	04-JAN-1994; 94WO-US00119.	
XX		
PR	04-JAN-1993; 93US-0001738.	
PA	(SYN-) SYNAPTIC PHARM CORP.	
XX		
FI	Borden LA, Smith KE, Weinsbank RL;	
XX		
DR	WPI: 1994-248881/30.	
XX	N-PSDB; AAQ65982.	
XX		
PT	Isolated nucleic acid encoding mammalian betaine-gamma-	

PT amino:butyric acid transporter - useful to detect and treat
 PT abnormalities associated with transporter expression
 XX
 PS
 SQ Claim 35; Fig 1; 91pp; English.

CC A betaine transporter, cloned from MDCK dog kidney cells, has been
 CC isolated (Ramuchel et al., J. Biol. Chem. 267 (1):649-652).
 CC Betaine is an important osmolyte in the kidney, and possibly other
 CC organs. This transporter was found to have higher affinity for
 CC GABA than for betaine, suggesting a role in GABAergic transmission.
 CC A related clone from a human brain cDNA library has now been
 CC isolated (AA066982). Although the function of this transporter
 CC in the nervous system is not understood, it may serve to regulate
 CC both GABAergic transmission and osmolarity.
 CC Gene prods. may be used in the detection or treatment of epilepsy,
 CC migraine, ischaemia, myoclonus, spasticity or chronic pain.
 CC
 SQ Sequence 614 AA;

Query Match 100.0%; Score 75; DB 15; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
 |||||
 DB 583 KOHPCLDGSAGRN 595

RESULT 2
 AAR89481
 ID AAR89481 standard; Protein; 614 AA.

AC AAR89481;
 XX
 DT 30-MAY-1996 (first entry)
 XX
 DE Human betaine/GABA transporter.
 DE
 XX Betaine/GABA transporter; gamma-aminobutyric acid;
 KW neuropsychiatric disorders; human; rat; epilepsy; anxiety.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO9604790-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 16-AUG-1995; 95WO-US10579.
 XX
 PS 16-AUG-1994; 94US-0291299.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Borden LA, Smith KE, Weinschank RL;
 XX
 DR WPI; 1996-139355/14.
 DR N-PSDB: AAT16542.
 XX
 PT Mammalian betaine gamma-aminobutyric acid transporter DNA - used to
 PT develop prods. for the study, diagnosis and therapy of GABA
 PT associated abnormalities; partic. neuro-psychiatric disorders.
 PT
 XX
 PS Disclosure; Fig 1A-D; 191pp; English.

CC The DNA (AAT16542) encoding the human betaine/GABA transporter was
 CC isolated from a human striatum cDNA library using probes (AAT16538
 CC to AAT16541) based on a rat GABA transporter (GAT-2) cDNA.
 CC The region of rat betaine/GABA transporter encoded by the
 CC sequence given in AAT16543 corresponds to amino acids 84-139 of
 CC the human betaine/GABA transporter.
 CC Mammalian betaine gamma-aminobutyric acid transporter DNA and
 CC related prods. may be used for the study, diagnosis and therapy
 CC of GABA associated abnormalities, partic. neuropsychiatric

CC disorders, such as epilepsy and anxiety.
 XX
 PS
 SQ Sequence 614 AA;

Query Match 100.0%; Score 75; DB 17; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOHPCLDGSAGRN 13
 |||||
 DB 583 KOHPCLDGSAGRN 595

RESULT 3
 ABG21342
 ID ABG21342 standard; Protein; 1923 AA.

AC ABG21342;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21333.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200175067-A2
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB: AAS85529.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 XX
 PS Claim 20; SEQ ID NO 51701; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX

PT Tourette's disorder, angina and leukaemia -

XX Claim 1: Page 99-100; 130pp; English.
 PS
 CC The present sequence represents a human transmembrane proteins (HTMP).
 CC Agonists and antagonists of the protein are used to treat a disease
 CC or condition associated with overexpression of the protein. Diseases
 CC and conditions which can be treated include cell proliferative,
 CC immunological, reproductive, smooth muscle and neurological disorders
 CC e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency
 CC syndrome (AIDS), allergies, ovulatory defects, angina, hypertension,
 CC stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The
 CC polynucleotides may be used to detect and quantify gene expression in
 CC biopsied tissues where protein expression may be correlated with disease
 CC e.g. to determine absence, presence or excess expression of HTMP or to
 CC monitor regulation of HTMP expression during therapeutic intervention.
 CC
 SQ Sequence 374 AA:
 Query Match 56.0%; Score 42; DB 21; Length 374;
 Best Local Similarity 72.7%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 KOHPCLDGSG 11
 |||||
 114 KOHPLDGVNG 124
 DB
 RESULT 6
 ABB59371
 ID ABB59371 standard; Protein; 4601 AA.
 AC
 XX ABB59371:
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 4905.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001MO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PA 11-JUL-2000; 2000US-0614150.
 XX
 PI (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL03474.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Disclosure: SEQ ID NO 4905; 21pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 4601 AA:
 Query Match 56.0%; Score 42; DB 22; Length 4601;
 Best Local Similarity 63.6%; Pred. No. 66+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 3 HPCLDGSGRN 13
 |||||
 439 HPCRDNNAGCN 449
 DB
 RESULT 7
 ABG08064
 ID ABG08064 standard; Protein; 149 AA.
 AC
 XX ABG08064:
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #8055.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PA 23-AUG-2000; 2000US-0649167.
 XX
 PI (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72251.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS
 PS Claim 20; SEQ ID NO 38423; 103pp; English.
 PS
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 149 AA:
SQ Query Match 54.7%; Score 41; DB 22; Length 149;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSAGRN 13
||| | : | |
Db 69 HPCLDGAPVRN 79

RESULT 8
AAU46916
ID AAU46916 standard; Protein; 174 AA.
XX AAU46916;
XX 27-FEB-2002 (first entry)
XX Propionibacterium acnes immunogenic protein #7812.
DE SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX Propionibacterium acnes.
OS WO200181581-A2.
XX 01-NOV-2001.
XX 20-APR-2001; 2001WO-US12865.
XX 21-APR-2000; 2000US-199047P.
XX 02-JUN-2000; 2000US-208841P.
XX 07-JUL-2000; 2000US-216747P.
XX (CORI-) CORIXA CORP.
XX Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59535.
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris -
XX Example 1; SEQ ID No 811; 1069pp; English.
XX Sequences AAU93105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA).
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 174 AA:
SQ Query Match 54.7%; Score 41; DB 22; Length 174;
Best Local Similarity 54.5%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 HPCLDGSAGRN 13
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Db 77 HPCVEROAGEN 87

RESULT 9
ABB62080
ID ABB62080 standard; Protein; 319 AA.
XX ABB62080;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 13032.
DE Drosophila: developmental biology; cell signalling; insecticide;
XX pharmacological.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL06183.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Disclosure: SEQ ID NO 13032; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
XX sequences (ABU01840-ABU16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.

SO Sequence 319 AA:
Query Match 54.7%; Score 41; DB 22; Length 319;
Best Local Similarity 58.3%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KOHCLDGSAGR 12
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Db 249 RRHCLTDSNGR 260

RESULT 10

AAG04837
ID AAG04837 standard; Protein; 232 AA.
XX
AC AAG04837;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1014.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
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XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
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XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
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XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
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XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
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XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
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PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
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PR 19-JUL-1999; 99US-0144332.
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PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.

DE	Arabidopsis thaliana protein fragment SEQ ID NO: 1013.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PE	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
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PR	31-AUG-1999;	9905-0151438.
PR	01-SEP-1999;	9905-0151930.
PR	07-SEP-1999;	9905-0152363.
PR	10-SEP-1999;	9905-0153070.
PR	13-SEP-1999;	9905-0153758.
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PR	29-OCT-1999;	9905-0162142.

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Best Local Similarity		40.9%;	Pred. No. 51;		
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ID	AAG04835 standard; Protein:	329 AA.			
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AC	AAG04835;				
XX					
DT	17-OCT-2000 (first entry)				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 1012.				
XX					
KW	Protein identification: signal transduction pathway; metabolic pathway;				
KM	hybridisation assay; genetic mapping; gene expression control; promoter;				
XX	termination sequence.				
OS	Arabidopsis thaliana.				

XX XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0122548.
PR 23-MAR-1999; 99US-0125788.
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PR 08-APR-1999; 99US-0128714.
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PR 03-JUN-1999; 99US-0137528.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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PR 16-JUN-1999; 99US-0139452.
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XX	Human nervous system related polypeptide SEQ ID NO 4633.				
XX					
XX	Human: neoptropic; neuroprotective; cytostatic; dermatological; virocidic;				
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;				
KW	antiparkinsonian; antischizy; antinaemic; antiarthritic; cancer;				
KW	antipneumatic; hepatotropic; cerebroprotective; antiinflammatory;				
KW	antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;				
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;				
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine.				
XX					
XX					
XX	Homo sapiens.				
XX					
XX	MO200159063-A2.				
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR
XX
PA (HUMA-) HUMAN GENOME SCL INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI, 2001-541565/60.

DR N-PSDB; ABA12302.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Claim 11; SEQ ID NO 4633; 1701bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABA1678-ABA1800) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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SQ Sequence 72 AA:

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DB 34 HPCLEGQA 41
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RESULT 14
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AC AAM87341;
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DT 07-NOV-2001 (first entry)
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XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM.
XX
XX WPI; 2001-483426/52.
DR N-PSDB; AAK60122.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX
XX ClalM 11; SEQ ID NO 14934; 3071bp + Sequence Listing; English.
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting

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